

Search completed: August 10, 2004, 16:44:40
Job time : 14.5 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:36:04 ; Search time 8 Seconds
(without alignments)

1223.649 Million cell updates/sec

Title: US-09-811-367b-3

Perfect score: 1029

Sequence: 1 MADSSIVSTLELPEAPQVQD.....GLQASCEVALQWICKVKVLY 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 40997

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180.5	17.5	179	1	Q9mk9 macaca mula
2	178.5	17.3	179	1	Q13241 homo sapien
3	178.5	17.3	179	1	Q9mz41 pan troglod
4	152.5	14.8	146	1	IXB_TRIPL
5	150.5	14.6	148	1	CVXB_CRODU
6	146.5	14.2	163	1	V2339 FOWPV
7	145	14.1	146	1	MMHB_AGRHA
8	144	14.0	149	1	CLE2_HUMAN
9	139	13.5	157	1	MMHA_AGRHA
10	138	13.4	167	1	V008_FOWPV
11	125.5	12.2	133	1	RHCA_AGRKH
12	124.5	12.1	117	1	CHBB_CROHO
13	124.5	12.1	123	1	ABAA_TRIAB
14	120.5	11.7	158	1	CVXA_CRODU
15	119	11.6	133	1	BOTB_BOTJA
16	113.5	11.0	125	1	BOTB_BOTJA
17	110.5	10.7	155	1	PLC_HALLA
18	109.5	10.6	129	1	RHCB_AGRKH
19	108.5	10.5	125	1	ABAB_TRIAB
20	105	10.2	174	1	PAP3_MOUSE
21	104	10.1	152	1	IXA_TRIPL
22	103	10.0	175	1	PAP1_MOUSE
23	103	10.0	175	1	PAP2_MOUSE
24	102.5	10.0	162	1	LECB_MEGRO
25	101.5	9.9	123	1	ECHB_ECHCA
26	101.5	9.9	158	1	LECG_TRIST
27	101	9.8	175	1	PAP1_HUMAN
28	97.5	9.5	165	1	LITH_RAT
29	97	9.4	127	1	CHBA_CROHO
30	97	9.4	134	1	ABAA_TRIAB
31	97	9.4	135	1	LECG_CROAT
32	95	9.2	174	1	PAP3_RAT
33	94	9.1	175	1	PAP1_RAT

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34 93.5 9.1 118 1 ABBB_TRIAB P81116 trimeresuru
35 93 9.0 158 1 NKGF_PANTR Q95mil pan troglod
36 93 9.0 163 1 ANP_HEMAN P05140 hemitriptet
37 92 8.9 158 1 NKGF_HUMAN O43908 homo sapien
38 91 8.8 175 1 PBCG_MESAU Q92778 mesocricetu
39 90 8.7 166 1 LITA_HUMAN P05451 homo sapien
40 89.5 8.7 166 1 LITB_HUMAN P48304 homo sapien
41 86.5 8.4 133 1 ECHA_EHCA P81017 echis carin
42 86 8.4 135 1 LECG_BITAR Q9psn0 bitis carin
43 86 8.4 135 1 LECG_LACST Q9psm4 lacheis st
44 86 8.4 175 1 LITH_BOVIN P23132 bos taurus
45 85.5 8.3 132 1 ABBA_TRIAB P81115 trimeresuru

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ALIGNMENTS

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RESULT 1
CD94_MACMU
ID CD94_MACMU STANDARD; Q9MK7; Q9MZK8; PRT; 179 AA.
AC Q9MK7; Q9GK91; Q9MK7; Q9MZK8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1).
DE KURDI OR CD94.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20322487; PubMed=10866118;
RA LaBonte M.L., Levy D.B., Letvin N.L.;
RT "Characterization of rhesus monkey CD94/NKG2 family members and
RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,
RT and D.";
RL Immunogenetics 51:496-499(2000).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21158386; PubMed=11261935;
RA Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
RT "Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative
RT splicing of 5' exons in rhesus monkey decidua.";
RL Immunogenetics 53:69-73(2001).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q9MK9-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q9MK9-2; Sequence=VSP_003055;
CC Name=3; Synonyms=CD94 alt;
CC IsoId=Q9MK9-3; Sequence=VSP_003054;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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EMBL; AF190931; AAF74527.1; -.
EMBL; AF190932; AAF74528.1; -.

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DR EMBL; AF190933; AAF74529.1; -.
DR EMBL; AF294886; AAG34498.1; -.
DR HSP; P22897; LEGS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_C; 1.
DR SMART; SM0034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00411; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; Polymorphism.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 1 34 MAVERKTLRLSLSGTLGIICLSIMATIGILLKNS -> MAA
(in isoform 3).
FT FTID=VSP 003054.
FT L -> LQ (in isoform 2).
FT FTID=VSP_003055.
FT Y -> D.
FT VARIANT 139 139
FT SEQUENCE 179 AA; 20607 MW; 06212B4494527F07 CRC64;
Query Match 17.5%; Score 180.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. No. 66-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLTLVLSMLMYQLCGS-----KDTSCSHCPSCPILWTRNGS 84
Db 14 GLTGLICLSMATLIGLLKNSFTKLSVEPAYTPGPNILQKSDC--C-SCEKWGVRC 70
QY 85 HCIFYSMKKDNSSLKFCADKSGHLLTPDPNQGVKLFGXYLGQDFYIWLGNID---GW 141
Db 71 NCYFISSEKTNESRHFCAQSKSSLLQNRDELDFMSS--SQHFYIWLGLSYSEHTAM 128
QY 142 RWEQGPALSLRILTNSLI---ORCGAIHRNG-LQASSCEVALQWCKVKL 187
Db 129 LWENGSAQLFPLFPFETFKPKNCIAYNSKGNALDESCETKNRYICKQOL 178
RESULT 2
CD94 HUMAN
ID CD94 HUMAN STANDARD; PRT; 179 AA.
AC Q13241; O43321; O43773; Q9UBE3; Q9UEQ0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1) (KB43).
GN KLRD1 OR CD94.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=96011848; PubMed=7589107;
RA Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
RA Lanier L.L.;
TX TISSUE=Blood;
RX MEDLINE=96011848; PubMed=7589107;
RA Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
RA "Molecular characterization of human CD94: a type II membrane
RT glycoprotein related to the C-type lectin superfamily.";
RL Eur. J. Immunol. 25:2433-2437(1995).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98139529; PubMed=9472066;
RA Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,

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RA Leirach H., Francis F., Lopez-Botet M.;
RT "Structure of the human CD94 C-Type lectin gene.";
RL Immunogenetics 47:305-309(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Biassoni R.;
RN [4]
RP Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=98267245; PubMed=9601951;
RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,
RA Tohma S., Inoue T., Yamamoto K., Juji T.;
RT "A alternatively spliced form of the human CD94 gene.";
RL Immunogenetics 48:87-88(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Flaherty J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalinski D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q13241-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q13241-2; Sequence=VSP_003053;
CC Name=3; Synonyms=CD94 alt;
CC IsoId=Q13241-3; Sequence=VSP_003052;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd94.htm".
CC -----
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CC -----
CC EMBL; U30610; AAC50291.1; -.
CC EMBL; Y14287; CAA74663.1; -.
CC EMBL; Y14288; CAA74663.1; JOINED.
CC EMBL; AJ000673; CAA04230.1; -.
CC EMBL; AJ000001; CAA03845.1; -.
CC EMBL; AB009597; BAA24450.1; -.
CC EMBL; AB010084; BAA24451.1; -.
CC EMBL; BC028009; AAB28009.1; -.
CC PDB; 1B6E; 15-JUN-99.

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DR Genew; HGNC:6378; KLRD1.
DR MIM; 602894; -.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; 3D-structure.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 34 MAVFKTLWLKISGTGLGICLSMATLGLLKNS -> MAA
(in isoform 3).
FT VARSPLIC 105 105 /FTid=VSP_003052.
FT VARSPLIC 105 105 /FTid=VSP_003053.
FT SEQUENCE 179 AA; 20497 MW; 1884D99E8D9583A7 CRC64;
Query Match 17.3%; Score 178.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. No. 9.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIIICLSMATLGIILKNSFTKLSTEPATPGPNIELQKSDC--C-SQCKWVGRC 70
QY 85 HCYFYSMEKDWNSLKFCKADKSGHLLTFPDNQVKLFGEYLGDFYWGILRNID---GW 141
Db 71 NCYFISSEQKTWNEHRLCASQKSLQLQNTDELDFMSS--SQQFYWIGLSYEHTAW 128
QY 142 RWGGPALSRLITN---SLIQRCGATHRNG-LOASCEVALQWICKVIL 187
Db 129 LWNGSALSQYLPFPSTFNTKNCIAYNPNGNALDESCDKNRVICKQOL 178
RESULT 3
CD94_PANTR
ID _CD94_PANTR STANDARD; PRT; 179 AA.
AC Q9MZ41;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
lectin-like receptor subfamily D, member 1).
GN KLRD1 OR CD94.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20350666; PubMed=10894168;
RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
RA Muir D.G., Canavez F., Cooper S.L., Valliant N.M., Lanier L.L.,
RA Parham P.;
RT "Rapid evolution of NK cell receptor systems demonstrated by
comparison of chimpanzees and humans.";
RL Immunity 12:687-698(2000).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=21623889; PubMed=11751968;
RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
RT "Conservation and variation in human and common chimpanzee CD94 and
RT NKG2 genes.";
RL J. Immunol. 168:240-252(2002).
CC -I- FUNCTION: Plays a role as a receptor for the recognition of MHC
class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -I- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
members.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1; Synonyms=CD94-A;
IsoId=Q9MZ41-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
IsoId=Q9MZ41-2; Sequence=VSP_003056;
-TISSUE SPECIFICITY: Natural killer cells.
-SIMILARITY: Contains 1 C-type lectin family domain.
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CC EMBL; AF259054; AAF86964.1; -.
CC HSPB; P22897; IEHG.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
CC PROSITE; PS50041; C TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 105 105 /FTid=VSP_003056.
FT SEQUENCE 179 AA; 20493 MW; 7244D99E8D9587E7 CRC64;
Query Match 17.3%; Score 178.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. No. 9.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIIICLSMATLGIILKNSFTKLSTEPATPGPNIELQKSDC--C-SQCKWVGRC 70
QY 85 HCYFYSMEKDWNSLKFCKADKSGHLLTFPDNQVKLFGEYLGDFYWGILRNID---GW 141
Db 71 NCYFISSEQKTWNEHRLCASQKSLQLQNTDELDFMSS--SQQFYWIGLSYEHTAW 128
QY 142 RWGGPALSRLITN---SLIQRCGATHRNG-LOASCEVALQWICKVIL 187
Db 129 LWNGSALSQYLPFPSTFNTKNCIAYNPNGNALDESCDKNRVICKQOL 178
RESULT 4
IXB_TRIFL
ID _IXB_TRIFL STANDARD; PRT; 146 AA.
AC P23807; O91247;
DT 01-NOV-1991 (Rel. 20, Created)

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GO: GO:0007596; P:blood coagulation; IDA.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00334; CLECT_1.
 DR PROSITE: PS00615; C-TYPE LECTIN 1; 1.
 DR PROSITE: PS0041; C-TYPE LECTIN 2; 1.
 KW Blood coagulation; Lectin; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 146 MAMUSHIGIN BETA CHAIN.
 FT DOMAIN 32 143 C-TYPE LECTIN.
 FT DISULFID 25 36 BY SIMILARITY.
 FT DISULFID 53 142 BY SIMILARITY.
 FT DISULFID 98 98 INTERCHAIN (WITH C-103 IN ALPHA CHAIN)
 (BY SIMILARITY).
 FT DISULFID 119 134 (BY SIMILARITY).
 FT SEQUENCE 146 AA; 17064 MW; 9EDA84BDC24E76D CRC64;
 Query Match 14.1%; Score 145; DB 1; Length 146;
 Best Local Similarity 27.3%; Pred. No. 1.7e-07;
 Matches 45; Conservative 17; Mismatches 55; Indels 48; Gaps 8;
 QY 35 LSRFAMVALGLLTIVILMSILMYQRIILCCGSKDSTCSHCPCSPILWTRNGSHCHYFYSMEKK 94
 DB 1 MGRFTFLSGLLVFV-----SLSGTGADCPSD---WSSVEGHCYRFFQKEM 44
 QY 95 DWNSSLKFCAD--KGSHLLTFPDNQG---VKLFGEYLQDFYWGILGRNIDGW-----RW 143
 DB 45 TWEDAEEKCTQQRKESHLVSFHSSEVDVFSMTWPKLYDFVWGLANNI--WNECMVEM 102
 QY 144 EGGPALSRLILNLSLIQRCGAIHRNGLOASCEVAL-----QWICK 184
 DB 103 TDGTRLS-----HNAWITESECIAAKTTDNQWLSR 132
 RESULT 8
 CLE2_HUMAN
 ID CLE2_HUMAN STANDARD; PRT; 149 AA.
 AC Q92478; Q9BSV4; Q9UQB4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE C-type lectin superfamily member 2 (Activation-induced C-type lectin).
 GN CLECSF2 OR AICL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97190245; PubMed=9038101;
 RA Hanann J., Montgomery K.T., Lau S., Kucherlapati R., van Lier R.A.W.;
 RT "AICL, a new activation induced antigen encoded by the human NK gene
 complex.";
 RL Immunogenetics 45:295-300(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97173880; PubMed=10072769;
 RA Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.;
 RT "Selection of cDNAs encoding putative type II membrane proteins on the
 cell surface from a human full-length cDNA bank.";
 RL Gene 228:161-167(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Urinary bladder;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Expressed preferentially in lymphoid tissues,
 CC and in most hematopoietic cell types.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
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 CC
 DR EMBL; X96719; CAA65480.1; -;
 DR EMBL; AB015628; BAA76495.1; -;
 DR EMBL; BC005254; AAH05254.1; -;
 DR GenBank; HGNC:2053; CLECSF2.
 DR MIM; 603242; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005530; F:lectin; TAS.
 DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
 DR PROSITE; PS0041; C-TYPE LECTIN 2; 1.
 KW Glycoprotein; Transmembrane; Lectin; Signal-anchor.
 FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 8 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 FT DOMAIN 26 149 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 42 145 C-TYPE LECTIN.
 FT DISULFID 46 63 BY SIMILARITY.
 FT DISULFID 87 144 BY SIMILARITY.
 FT DISULFID 123 136 BY SIMILARITY.
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 79 79 M -> T (IN REF. 3).
 FT CONFLICT 107 107 D -> H (IN REF. 3).
 SQ SEQUENCE 149 AA; 17307 MW; 0B4FED23424F6C55 CRC64;
 Query Match 14.0%; Score 144; DB 1; Length 149;
 Best Local Similarity 26.5%; Pred. No. 2.2e-07;
 Matches 43; Conservative 28; Mismatches 67; Indels 24; Gaps 7;
 QY 34 HLSRFAMVALGLLTIVILMSILMYQRIILCCGSKDSTCSHCPCSPILWTRNGSHCHYFYSMEK 93
 DB 5 HKKCFIIVGV-LITNTIITIVKL-----TRDSQ-----SLCPYDWIGFQNKCYFSKEE 53
 QY 94 KDNWSSLKFCADKSHLLTFPDNQGKVLFGYLGQDFYWGIL---RNIDGWRWEGGPALS 150
 DB 54 GDNWSSKYNCTQHADLTIDINIEEMNPLRRYKCSSDHWIKLWAKNRTG-QWVDGAT-- 110
 QY 151 LRILTNLSLIQ-----CGAIHRNGLOASCEVALQWICKVLY 188
 DB 111 ---FTKSGFMRGSGCGAVLSDGGAATACATCYTERKWKCRKH 149
 RESULT 9
 MHA_AGHA


```
RHCA_AGRKH
ID RHCA_AGRKH STANDARD; PRT; 133 AA.
AC P81397;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Rhodocetin alpha subunit.
OS Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Calloselasma.
OX NCBI_TaxID=8717;
RN
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96420502; PubMed=823201;
RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
RA Smith A.I., Lopez J.A., Berndt M.C.;
RT "Binding of a novel 50-kilodalton albosaggregin from Trimeresurus
RT albobabris and related viper venom proteins to the platelet membrane
RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and
RT glycoprotein Ib-mediated platelet activation.";
RL Biochemistry 35:12629-12639(1996).
CC
CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system, inhibits vWF
CC binding, and stimulates agglutination.
CC
CC -!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
CC
CC -!- SUBCELLULAR LOCATION: Secreted.
CC
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR InterPro; IPR002353; AntifreezeII.
DR Pfam; PF00059; Lectin C; 1.
DR PRINTS; PRO0356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN 9 116 C-TYPE LECTIN.
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 115 BY SIMILARITY.
FT DISULFID 92 92 INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
(POTENTIAL).
FT DISULFID 95 107 BY SIMILARITY.
SQ SEQUENCE 117 AA; 13888 MW; 07835BBC861E9EAD CRC64;

Query Match 12.1%; Score 124.5; DB 1; Length 117;
Best Local Similarity 25.8%; Pred. No. 1.5e-05;
Matches 31; Conservative 23; Mismatches 51; Indels 15; Gaps 6;

QY 75 CPILWTRNGSHCYFMSKKDWSLKFCA--GSHLLTFPDNQGVKLFGEYLGQDFY 132
Db 2 CPDWSSTKSYCYRPFKEKKTWEAEAREFTQKEAHLVSM--ENRLEAVFDVMYNNFE 61
QY 133 IGLRNIDGW-----RWGGPALSRLIT--NSLIQRCGAIHRNGLOASSCEVALQWICK 184
Db 62 MGRDRI--WNERRLQWSDGTGVNYKAWSAEPCIV--CRATDQWL-STSCSKTHNVVCK 116

RESULT 13
ABM4_TRIAB STANDARD; PRT; 123 AA.
ID ABM4_TRIAB
AC P81114;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Albosaggregin A subunit 4.
OS Trimeresurus albobabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Albosaggregins A and B. Structure and interaction with human
RT platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC
CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC agglutination.
CC
CC -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
CC disulfide-linked.
CC
CC -!- SUBCELLULAR LOCATION: Secreted.
CC
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
```

```
DR HSP; P23807; 11XX.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW SIGNAL; 1 23
FT DOMAIN 1 121 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 119 BY SIMILARITY.
FT DISULFID 96 111 BY SIMILARITY.
SQ SEQUENCE 123 AA; 14365 MW; D4CFBEE1219C9BIE CRC64;

Query Match 12.1%; Score 124.5; DB 1; Length 123;
Best Local Similarity 25.6%; Pred. No. 1.6e-05;
Matches 31; Conservative 18; Mismatches 59; Indels 13; Gaps 4;

QY 75 CPILWTRNGSHCYFYSMEKKDWSLKECAD--KGSHLLTFPDNQ-----VKLFGEVLGQ 128
Db 2 CPDWSYEGHCYRVFNEPONWDAEKFCTQKHGSHLVFSQSSEADVVQVMTPTLNA 61
QY 129 DFYWIIGLRNIDGW-----RWEGGPALSLRLITNSLIQKCGAIHRNGLOASCEVALQWIC 183
Db 62 NLVWIGLSNL--WNQCNQSDSGTXLDYKXWREQFCGLVSRITNNEWLSMDCSTHSFVC 119
QY 184 K 184
Db 120 E 120

RESULT 14
CVXA_CRODU
ID CVXA_CRODU STANDARD; PRT; 158 AA.
AC O93426;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Convulxin alpha precursor (CVX alpha).
OS Crotalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8732;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 24-48; 61-68; 108-120; 139-145 AND
149-153.
RC TISSUE=Venom gland;
RX MEDLINE=98324901; PubMed=9657980;
RA Leduc M., Bon C.;
RT "Cloning of subunits of convulxin, a collagen-like platelet-
aggregating protein from Crotalus durissus terrificus venom.";
RL Biochem. J. 333:389-393(1998).
CC -1- FUNCTION: Binds to the platelet and collagen receptor,
glycoprotein VI (GPVI).
CC -1- SUBUNIT: Heterohexamer of three alpha chains and three beta
chains; disulfide-linked.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; Y16348; CAA76181.1; -.
DR HSP; P23806; 11XX.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; lectin_c; 1.

DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Lectin; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 158 CONVULXIN ALPHA.
FT DOMAIN 34 153 C-TYPE LECTIN.
FT DISULFID 27 38 BY SIMILARITY.
FT DISULFID 55 152 BY SIMILARITY.
FT DISULFID 104 104 INTERCHAIN (WITH C-100 IN BETA CHAIN)
(POTENTIAL).
FT DISULFID 127 144 BY SIMILARITY.
FT DISULFID 158 158 INTERCHAIN (WITH C-26 IN BETA CHAIN)
(POTENTIAL).
SQ SEQUENCE 158 AA; 18141 MW; 949F9C6D673E2318 CRC64;

Query Match 11.7%; Score 120.5; DB 1; Length 158;
Best Local Similarity 25.0%; Pred. No. 5.3e-05;
Matches 44; Conservative 26; Mismatches 57; Indels 49; Gaps 10;

QY 35 LSRFAMVALGLLTVILMSLIMYQRIILCCGSKDSTCHSPCPILWTRNGSHCYFYSMEKK 94
Db 1 MGRFIFVSGLL-VLFSL-----SGTGAGLHCPSD---WYYDDQHCYRIFNEEM 46
QY 95 DWNSSLKFCAD--KGSHLLTFPDNQGVKLFGEVLGQDFY-WIGLRNID----- 139
Db 47 NWEDAWEFCTKQAKGAHLVS-----IKSAKE---ADFVAMVMTQNTIESFSHVSIGLRV 97
QY 140 -----GWRWEGGPALSLRLITNSLIQRCGAIHR-NGLO---ASCEVALQWICK 184
Db 98 QNKEKQCTRWSDGSSVSDNLDLITKCSLLKKTGFRKMFVASCIGKIPFVCK 153

RESULT 15
BOTA_BOTJA
ID BOTA_BOTJA STANDARD; PRT; 133 AA.
AC P22029;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Botrocetin, alpha chain (Platelet coagglutinin).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=93157385; PubMed=8430107;
RA Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
Titani K.;
RT "Primary structure of two-chain botrocetin, a von Willebrand factor
modulator purified from the venom of Bothrops jararaca.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
RN [2]
SEQUENCE OF 1-40.
RC TISSUE=Venom;
RX MEDLINE=91129280; PubMed=1993206;
RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
Fukui H., Sugimoto M., Ruggeri Z.M.;
RT "Isolation and chemical characterization of two structurally and
functionally distinct forms of botrocetin, the platelet coagglutinin
isolated from the venom of Bothrops jararaca.";
RL Biochemistry 30:1957-1964(1991).
RN [3]
X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=22118144; PubMed=12121649;
RA Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
RT "Structural basis of von Willebrand factor activation by the snake
toxin botrocetin.";
```


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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:39:05 ; Search time 32 Seconds
(without alignments)
1853.669 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSYITLPEAPQVQD.....GLQASCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 396094

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1029	100.0	188	11	O88713	O88713 mus musculus
2	838	81.4	188	11	Q64335	Q64335 rattus norv
3	180	17.5	179	11	O54708	O54708 mus musculus
4	180	17.5	179	11	O54707	O54707 mus musculus
5	177.5	17.2	179	6	Q8MHV8	Q8MHV8 pongo pygma
6	174.5	17.0	179	6	Q8MJ13	Q8MJ13 pongo pygma
7	174.5	17.0	179	6	Q8MHY9	Q8MHY9 pongo pygma
8	171.5	16.7	179	6	Q8MJ14	Q8MJ14 pongo pygma
9	171.5	16.7	181	4	Q9NZS1	Q9NZS1 homo sapien
10	169	16.4	159	6	Q8SPX0	Q8SPX0 sus scrofa
11	168	16.3	165	11	Q9R007	Q9R007 mus musculus
12	163.5	15.9	146	13	Q9IAM0	Q9IAM0 agkistrodon
13	163.5	15.9	146	13	Q8J1W1	Q8J1W1 agkistrodon
14	163	15.8	161	6	Q95JG4	Q95JG4 bos taurus
15	161	15.6	165	6	Q9GLF4	Q9GLF4 sus scrofa
16	159.5	15.5	132	11	Q8R4K5	Q8R4K5 rattus norv

17	159.5	15.5	164	11	Q8BL24	Q8BL24 mus musculus
18	158.5	15.4	146	13	Q8AYA4	Q8AYA4 agkistrodon
19	156	15.2	163	6	Q9GK90	Q9GK90 macaca mla
20	154	15.0	148	13	Q8AV98	Q8AV98 trimeresuru
21	153	14.9	179	11	O35778	O35778 rattus norv
22	150	14.6	185	6	Q9GLF3	Q9GLF3 sus scrofa
23	148.5	14.4	146	13	Q8JGT6	Q8JGT6 trimeresuru
24	148	14.4	154	4	Q8WUP7	Q8WUP7 homo sapien
25	146.5	14.2	146	13	Q9I840	Q9I840 agkistrodon
26	146.5	14.2	146	13	Q7T045	Q7T045 vipera lebe
27	145.5	14.1	185	6	Q9MZJ6	Q9MZJ6 macaca mla
28	145	14.1	162	6	Q8MHY4	Q8MHY4 pongo pygma
29	145	14.1	173	4	Q9HD37	Q9HD37 homo sapien
30	144.5	14.0	146	13	Q9DG31	Q9DG31 agkistrodon
31	144	14.0	149	13	Q8UVC7	Q8UVC7 agkistrodon
32	143.5	13.9	188	4	Q9NY25	Q9NY25 homo sapien
33	143	13.9	149	13	Q8AYA3	Q8AYA3 agkistrodon
34	141.5	13.8	146	13	Q9DEA1	Q9DEA1 agkistrodon
35	140	13.6	145	13	Q9YGN4	Q9YGN4 agkistrodon
36	139	13.5	162	6	Q8MCH4	Q8MCH4 pongo pygma
37	139	13.5	162	6	Q8MCH3	Q8MCH3 pongo pygma
38	139	13.5	178	11	Q9LZW9	Q9LZW9 mus musculus
39	138.5	13.5	183	6	Q95J54	Q95J54 pan troglod
40	137.5	13.4	146	13	Q8JIV7	Q8JIV7 agkistrodon
41	137	13.3	187	4	Q9UKQ0	Q9UKQ0 homo sapien
42	136.5	13.3	158	13	Q8UVC6	Q8UVC6 agkistrodon
43	136.5	13.3	158	13	Q8AYA5	Q8AYA5 agkistrodon
44	135.5	13.2	146	13	Q9DEF8	Q9DEF8 agkistrodon
45	135	13.1	142	11	Q8CJ86	Q8CJ86 mus musculus

ALIGNMENTS

RESULT 1

O88713	PRELIMINARY;	PRT; 188 AA.
ID	O88713	
AC	O88713	
DT	01-NOV-1998 (TREMBlrel. 08, Created)	
DT	01-AUG-1999 (TREMBlrel. 11, Last sequence update)	
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)	
DE	Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor Gl).	
DE	like receptor Gl).	
GN	KLRG1 OR MAFA.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]_TaxID=10090;	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C.B-17 SCID;	
RX	MEDLINE=99077194; PubMed=9862378;	
RA	Hanke T., Corral L., Vance R.E., Raullet D.H.;	
RT	"2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type	
RT	II transmembrane receptor expressed by natural killer cells.";	
RL	Bar. J. Immunol. 28:409-441(1998).	
RN	[2]	
RP	SEQUENCE OF 2-188 FROM N.A.	
RA	Blaser C.;	
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=129/SvevTAcBr; TISSUE=Spleen;	
RX	MEDLINE=21115136; PubMed=11220622;	
RA	Voehringer D., Kaufmann M., Pircher H.;	
RT	"Genomic structure, alternative splicing, and physical mapping of the	
RT	killer cell lectin-like receptor Gl gene (KLRG1), the mouse homologue	
RT	of MAFA.";	
RL	Immunogenetics 52:206-211(2001).	
DR	EMBL; AF097357; AAC03718.1; -	
DR	EMBL; AJ010751; CAA09342.1; -	
DR	EMBL; AF317727; AAK40082.1; -	
DR	MGI; 1355294; Klrcl.	

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DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match 100.0%; Score 1029; DB 11; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSISTLELPEAPOQVDSRWKLVKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRI 60
DB 1 MADSSISTLELPEAPOQVDSRWKLVKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRI 60
QY 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTFFDNQGVK 120
DB 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTFFDNQGVN 120
QY 121 LFGYLGQDFYWGILNRIDGWRWEGGPPALSRLITNSLIQRCGAHNRNGLOASCEVALQ 180
DB 121 LFGYLGQDFYWGILNRIDGWRWEGGPPALSRLITNSLIQRCGAHNRNGLOASCEVALQ 180
QY 181 WICKKVL 187
DB 181 WICKKVL 187

RESULT 3
O54708 PRELIMINARY; PRT; 179 AA.
AC O54708;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD94.
GN KLRD1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB.17 SCID;
RX MEDLINE=98124458; PubMed=9464811;
RA Vance R.E., Tanamachi D.M., Hanke T., Raulat D.H.;
RT "Cloning of a mouse homolog of CD94 extends the family of C-type
RT lectins on murine natural killer cells.";
RL Eur. J. Immunol. 27:3236-3241(1997).
DR EMBL; AF030312; AAC28244.1; -.
DR MGD; MGI:1196275; Klrcl.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00022; EGF_1; 1.
SQ SEQUENCE 179 AA; 20809 MW; D59E1CB6G3139E45 CRC64;

Query Match 17.5%; Score 180; DB 11; Length 179;
Best Local Similarity 31.8%; Pred. No. 9.2e-11;
Matches 57; Conservative 25; Mismatches 75; Indels 22; Gaps 9;

QY 22 SRWLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIICGSKDST----CSHCPCSP 76
DB 7 TRWLMSVIFGK-CLFLMVLG---VLLINSFIQIQTSPPTTTFEVEQSECCVCL 62
QY 77 ILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTFFDNQGVKLFGEYLGQDFYWGIL- 135
DB 63 DKWVGHCQNCYFISKEEKSWERSDFCASQNSLLQ-PQSRNELSPMNF-SQTFWIGMH 120
QY 136 ---RNIDGWRWEGGPPALSRLITNSLIQRCGAHNRNGLOASCEVALOWICKV 186
DB 121 YSEKRN--AWLWEDGTVPKDLFFEFVIRPEHCIVYSPKSVSAESCENKRYICKKL 177

RESULT 4
O54707 PRELIMINARY; PRT; 179 AA.
AC O54707;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match 81.4%; Score 838; DB 11; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.5e-79;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
```



```

Db      14 GTLGIICLSMATIGILLKNSFTKLSIEPAFTPGDIELQKSDC--C-SQEKWVGVC 70
Qy      85 HCIFYSEKMDNSSLKFCADKGSLLTFPPNQGVKLFGEYLGQDFYWGIRNID---GW 141
Db      71 NCYFISSEKQWNSRHLCSQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
Qy      142 RWEGGPALS---LRILTNLSLQRCGAHRNG-LQASCEVALQWICKVL 187
Db      129 LWENGSSLSQYLFPLFETFPNFCIAYPNPNGNALDESCEDKNRYICKQOL 178

RESULT 7
Q8MHY9 PRELIMINARY; PRT; 179 AA.
AC Q8MHY9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Natural killer cell receptor.
GN POPY-CD94.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2207192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229 (2002).
DR EMBL; AF470380; AAM78485.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20520 MW; 6744895FBD95CFA CRC64;

Query Match 17.0%; Score 174.5; DB 6; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.4e-10;
Matches 54; Conservative 15; Mismatches 70; Indels 31; Gaps 7;

Qy      44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCPILWTRNGS 84
Db      14 GTLGIICLSMATIGILLKNSFTKLSIEPAFTPGDIELQKSDC--C-SQEKWVGVC 70
Qy      85 HCIFYSEKMDNSSLKFCADKGSLLTFPPNQGVKLFGEYLGQDFYWGIRNID---GW 141
Db      71 NCYFISSEKQWNSRHLCSQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
Qy      142 RWEGGPALS---LRILTNLSLQRCGAHRNG-LQASCEVALQWICKVL 187
Db      129 LWENGSSLSQYLFPLFETFPNFCIAYPNPNGNALDESCEDKNRYICKQOL 178

RESULT 8
Q8MJ14 PRELIMINARY; PRT; 179 AA.
AC Q8MJ14;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Natural killer cell receptor.
GN POPY-CD94.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2207192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229 (2002).
DR EMBL; AF470380; AAM78485.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20520 MW; 6744895FBD95CFA CRC64;

Query Match 17.0%; Score 174.5; DB 6; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.4e-10;
Matches 54; Conservative 15; Mismatches 70; Indels 31; Gaps 7;

Qy      44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCPILWTRNGS 84
Db      14 GTLGIICLSMATIGILLKNSFTKLSIEPAFTPGDIELQKSDC--C-SQEKWVGVC 70
Qy      85 HCIFYSEKMDNSSLKFCADKGSLLTFPPNQGVKLFGEYLGQDFYWGIRNID---GW 141
Db      71 NCYFISSEKQWNSRHLCSQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
Qy      142 RWEGGPALS---LRILTNLSLQRCGAHRNG-LQASCEVALQWICKVL 187
Db      129 LWENGSSLSQYLFPLFETFPNFCIAYPNPNGNALDESCEDKNRYICKQOL 178

RESULT 9
Q9NZS1 PRELIMINARY; PRT; 181 AA.
AC Q9NZS1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Lectin-like receptor FL, splice variant 1 KLRFl-sl.
GN KLRFl.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KIRFl, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576 (2000).
DR EMBL; AF175207; AAF37805.1; -.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CAE1E551 CRC64;

Query Match 16.7%; Score 171.5; DB 4; Length 181;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2207192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229 (2002).
DR EMBL; AF470383; AAM78483.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20536 MW; 6744895EC6F8780 CRC64;

Query Match 16.7%; Score 171.5; DB 6; Length 179;
Best Local Similarity 31.2%; Pred. No. 7.1e-10;
Matches 53; Conservative 16; Mismatches 70; Indels 31; Gaps 7;

Qy      44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCPILWTRNGS 84
Db      14 GTLGIICLSMATIGILLKNSFTKLSIEPAFTPGDIELQKSDC--C-SQEKWVGVC 70
Qy      85 HCIFYSEKMDNSSLKFCADKGSLLTFPPNQGVKLFGEYLGQDFYWGIRNID---GW 141
Db      71 NCYFISSEKQWNSRHLCSQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
Qy      142 RWEGGPALS---LRILTNLSLQRCGAHRNG-LQASCEVALQWICKVL 187
Db      129 LWENGSSLSQYLFPLFETFPNFCIAYPNPNGNALDESCEDKNRYICKQOL 178

RESULT 9
Q9NZS1 PRELIMINARY; PRT; 181 AA.
AC Q9NZS1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Lectin-like receptor FL, splice variant 1 KLRFl-sl.
GN KLRFl.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KIRFl, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576 (2000).
DR EMBL; AF175207; AAF37805.1; -.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CAE1E551 CRC64;

Query Match 16.7%; Score 171.5; DB 4; Length 181;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:35:35 ; Search time 47.5 Seconds
(without alignments)
1118.293 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSYSTLELPEAPQVD.....GLQASCEVALQWICKVLY 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1082526

Minimum DB seq length: 0
Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1029	100.0	188	4	AAE11760
2	838	81.4	188	2	AAR77033
3	838	81.4	188	2	AAW88277
4	838	81.4	188	4	AAE11761
5	551	53.5	114	2	AAR77472
6	222.5	21.6	99	2	AAW88267
7	178.5	17.3	179	2	AAW64791
8	178.5	17.3	179	2	AAW40222
9	178.5	17.3	179	8	AD676965
10	167.5	16.3	142	4	AAW80296
11	167.5	16.3	142	6	ABG72616
12	167.5	16.3	160	4	AAW80302
13	160.5	15.6	181	2	AAW72288
14	160.5	15.6	181	7	ADC38664
15	156	15.2	182	4	AAU19660
16	156	15.2	182	5	ABP47880
17	156	15.2	182	7	ADC10842
18	154	15.0	165	4	AAU00673
19	154	15.0	165	6	ABO32541
20	148.5	14.4	94	4	AAU19816
21	148.5	14.4	94	5	ABP48036
22	148.5	14.4	94	7	ADC10998
23	148.5	14.4	140	4	AAU19836
24	148.5	14.4	140	4	AAU19690
25	148.5	14.4	140	4	ABBI5422

ALIGNMENTS

RESULT 1

AAE11760
ID AAE11760 standard; protein; 188 AA.

XX AC AAE11760;

XX DT 18-DEC-2001 (first entry)

XX DE Mouse mast cell function associated antigen (MAFA) protein.

XX KW Mouse; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.

XX OS Mus sp.

XX PH Key Location/Qualifiers

XX FT Domain 64..188 /note= "Extracellular domain"

XX XX WO200170805-A2.

XX XX 27-SEP-2001.

XX XX 16-MAR-2001; 2001WO-US008596.

XX XX 17-MAR-2000; 2000US-0190716P.

XX XX (GEMI-) GEMINI SCI INC.

XX XX Takahashi N, Mikayama T;

XX XX WPI; 2001-611482/70.

XX XX N-PSDB; AAD18735.

XX XX Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.

XX XX Example 1; Page 19; 49pp; English.

XX XX The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical

26 148.5 14.4 140 4 ABB17909
27 148.5 14.4 140 5 ABP48056
28 148.5 14.4 140 5 ABP47910
29 148.5 14.4 140 7 ADC10872
30 148.5 14.4 140 7 ADC11018
31 148 14.4 149 2 AAW36957
32 147 14.3 35 4 AAM14192
33 147 14.3 35 4 ABB31139
34 147 14.3 35 4 AAM26602
35 147 14.3 35 4 ABB27967
36 147 14.3 35 4 ABB18604
37 147 14.3 35 4 AAM66323
38 147 14.3 35 4 AAM53935
39 147 14.3 35 4 ABG47989
40 147 14.3 35 4 AAM01928
41 147 14.3 35 5 ABG35971
42 145 14.1 145 4 AAU00675
43 145 14.1 145 6 ABO32547
44 145 14.1 146 4 AAM25760
45 144.5 14.0 146 4 AAM51544

Abb17909 Human ner
Abp48056 Human pol
Abp47910 Human pol
Adc10872 Human ext
Adc11018 Human pro
Aaw36957 Protein e
Aam14192 Peptide #
Abb31139 Peptide #
Aam26602 Peptide #
Abb27967 Human pep
Abb18604 Protein #
Aam66323 Human don
Aam53935 Human bra
Abg47989 Human liv
Aam01928 Peptide #
Abg35971 Human pep
Aau00675 Human INT
Abo32547 Secreted
Aam25760 Human pro
Aam51544 Snake ven

CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is mouse MAFA protein
 XX
 SQ

Query Match 100.0%; Score 1029; DB 4; Length 188;
 Best Local Similarity 100.0%; Pred. No. 6.6e-103;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSSYSTLELPEAPOQVDSRWKLVKAVLHRPHLSRFAMVALGLTIVILMSLLMYQRIL 60
 Db 1 MADSSYSTLELPEAPOQVDSRWKLVKAVLHRPHLSRFAMVALGLTIVILMSLLMYQRIL 60
 Qy 61 CCGSKDSTCSHCPCPILWTRNGSHCYVFSMEKDWNSLKFCDKSGSHLLTFPDNGVK 120
 Db 61 CCGSKDSTCSHCPCPILWTRNGSHCYVFSMEKDWNSLKFCDKSGSHLLTFPDNGVK 120
 Qy 121 LFGYLGQDFYWGIRNIDGWRWEGGPALSLRIITNSLIQRCGAHNRGLQASCEVALQ 180
 Db 121 LFGYLGQDFYWGIRNIDGWRWEGGPALSLRIITNSLIQRCGAHNRGLQASCEVALQ 180
 Qy 181 WICKKVL 188
 Db 181 WICKKVL 188

RESULT 2
 AAR77033
 ID AAR77033 standard; protein; 188 AA.

XX AAR77033;
 XX 01-FEB-1996 (first entry)
 XX Mammalian mast cell function-associated antigen (MAFA).
 XX Mast cell function-associated antigen; MAFA; soluble; ligand;
 XX identification; screening; inflammation; inflammatory; allergy; allergic;
 XX prevention.

XX Rattus rattus.
 XX WO9527734-A1.
 XX 19-OCT-1995.
 XX 06-APR-1995; 95WO-US004258.
 XX 08-APR-1994; 94IL-00109257.
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX (RYCU/) RYCU A.

XX Pecht I, Guthmann MD, Tal M;
 XX WPI; 1995-366356/47.
 XX N-PSDB; AAT01471.

XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
 XX useful for screening for ligands of MAFA which are useful for prevention
 XX of inflammatory and allergic reactions.

XX Claim 12; Page 37; 54pp; English.

XX A soluble form of mast cell function-associated antigen (MAFA) can be
 CC produced by recombinant techniques for use in the ligand- screening
 CC assay. The ligands that are identified may be used alone or in

CC combination with the MAFA to prevent inflammatory and allergic reactions
 XX
 SQ Sequence 188 AA;

Query Match 81.4%; Score 838; DB 2; Length 188;
 Best Local Similarity 80.7%; Pred. No. 3.2e-82;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MADSSYSTLELPEAPOQVDSRWKLVKAVLHRPHLSRFAMVALGLTIVILMSLLMYQRIL 60
 Db 1 MADNSIYSTLELPEAPRVQDDSRWKVAVLHRPCVSYLVVVALGLTIVILMSLLYQRTL 60
 Qy 61 CCGSKDSTCSHCPCPILWTRNGSHCYVFSMEKDWNSLKFCDKSGSHLLTFPDNGVK 120
 Db 61 CCGSKGFMCSQCPCPNLWNRNGSHCYVFSMEKDWNSLKFCDKSGSHLLTFPDNGVN 120
 Qy 121 LFGYLGQDFYWGIRNIDGWRWEGGPALSLRIITNSLIQRCGAHNRGLQASCEVALQ 180
 Db 121 LFGYVGEDFYWIGLRIDGWRWEDGPALSLILSNVYQCGTIHRCGLHASSCEVALQ 180
 Qy 181 WICKKVL 187
 Db 181 WICKKVL 187

RESULT 3
 AAW88277
 ID AAW88277 standard; protein; 188 AA.

XX AAW88277;
 XX 29-MAR-1999 (first entry)
 XX Rat mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA; splice variant; rat;
 XX inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

XX Rattus sp.

XX Key Location/Qualifiers
 XX Modified-site 82.84
 XX Modified-site /note= "Asn is N-glycosylated"
 XX Modified-site 97.99
 XX Modified-site /note= "Asn is N-glycosylated"

XX WO9854209-A2.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-GB001572.

XX 31-MAY-1997; 97GB-00011148.

XX (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

XX WPI; 1999-059806/05.

XX N-PSDB; AAW84222.

XX New polypeptide having a sequence corresponding to human mast cell
 XX function-associated antigen - useful in forming and manufacturing
 XX pharmaceutical compositions in the treatment of inflammatory and allergic
 XX diseases, and tumour growth.

XX Disclosure; Fig 4; 4pp; English.

XX This is the amino acid sequence of rat mast cell function-associated
 CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and
 CC basophils. The invention relates to cloning of the human MAFA molecule
 CC (see AAW8265) and to the discovery of splice variants (see AAW8266-67)
 CC of human MAFA that are not found in rat. Polypeptides and synthetic

CC peptides (see AA88258-64) based on human MAFA and human truncated MAFA,
 CC and polynucleotides encoding them, can be used in methods for the
 CC treatment of inflammatory and allergic diseases (e.g. rheumatoid
 CC arthritis and asthma), and tumour growth
 XX
 SQ Sequence 188 AA;

Query Match 81.4%; Score 838; DB 2; Length 188;
 Best Local Similarity 80.7%; Pred. No. 3.2e-82;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
 QY 1 MADSSYSTLELPEAPOQVDSRWKLVKAVLRPHLSRFAMVALGLLTVILMSLIMYQRIIL 60
 Db 1 MADNSYSTLELPAAPRVQDSSRWKLVKAVLRPHLSRFAMVALGLLTVILMSLIMYQRIIL 60
 QY 61 CCCKSDSTCHSCSPILWTRNGSHCYFFSMKKDWNSSLKFCADKSGSHLLTFPDNGVK 120
 Db 61 CCCKSGPMSCQCRCPNLMWRNGSHCYFFSMKKDWNSSLKFCADKSGSHLLTFPDNGVN 120
 QY 121 LFGYILGQDFYWIGLRNIDGWRWEGGPAISLRLITNSLIQRCGAIHNGIQAASCEVALQ 180
 Db 121 LFGYIVGEDFYWIGLRIDGWRWEDGPAISLILSNVQKGTIHRGGLHSCSEVALQ 180
 QY 181 WICKKVL 187
 Db 181 WICKKVL 187

RESULT 4
 AAE11761
 ID AAE11761 standard; protein; 188 AA.
 XX
 AC AAE11761;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Rat mast cell function associated antigen (MAFA) protein.
 XX
 DE Rat; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 XX
 OS Rattus norvegicus.
 XX
 PN WC200170805-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 16-MAR-2001; 2001WO-US008596.
 XX
 PR 17-MAR-2000; 2000US-0190716P.
 XX
 PA (GEMI-) GEMINI SCI INC.
 XX
 PI Takahashi N, Mikayama T;
 XX
 DR WPI; 2001-611482/70.
 DR N-PSDB; AAD18736.
 XX
 PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX
 PS Example 1; Page 19; 49pp; English.

XX The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition

CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is rat MAFA protein
 XX
 SQ Sequence 188 AA;

Query Match 81.4%; Score 838; DB 4; Length 188;
 Best Local Similarity 80.7%; Pred. No. 3.2e-82;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
 QY 1 MADSSYSTLELPEAPOQVDSRWKLVKAVLRPHLSRFAMVALGLLTVILMSLIMYQRIIL 60
 Db 1 MADNSYSTLELPAAPRVQDSSRWKLVKAVLRPHLSRFAMVALGLLTVILMSLIMYQRIIL 60
 QY 61 CCCKSDSTCHSCSPILWTRNGSHCYFFSMKKDWNSSLKFCADKSGSHLLTFPDNGVK 120
 Db 61 CCCKSGPMSCQCRCPNLMWRNGSHCYFFSMKKDWNSSLKFCADKSGSHLLTFPDNGVN 120
 QY 121 LFGYILGQDFYWIGLRNIDGWRWEGGPAISLRLITNSLIQRCGAIHNGIQAASCEVALQ 180
 Db 121 LFGYIVGEDFYWIGLRIDGWRWEDGPAISLILSNVQKGTIHRGGLHSCSEVALQ 180
 QY 181 WICKKVL 187
 Db 181 WICKKVL 187

RESULT 5
 AAR77472
 ID AAR77472 standard; protein; 114 AA.
 XX
 AC AAR77472;
 XX
 DT 01-FEB-1996 (first entry)
 XX
 DE Partial sequence of mast cell function-associated antigen (MAFA).
 XX
 KW Mast cell function-associated antigen; MAFA; soluble; ligand;
 KW identification; screening; inflammation; inflammatory; allergy; allergic;
 KW prevention.
 XX
 OS Rattus rattus.
 XX
 PN WO9527734-A1.
 XX
 PD 19-OCT-1995.
 XX
 PF 06-APR-1995; 95WO-US004258.
 XX
 PR 08-APR-1994; 94IL-00109257.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (RYCU/) RYCUS A.
 XX
 PI Pecht I, Guthmann MD, Tal M;
 XX
 DR WPI; 1995-366356/47.
 DR N-PSDB; AAT01471.

XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
 PT useful for screening for ligands of MAFA which are useful for prevention
 PT of inflammatory and allergic reactions.

XX Disclosure; Page 38; 54pp; English.

XX A soluble form of mast cell function-associated antigen (MAFA) can be
 CC produced by recombinant techniques for use in the ligand- screening
 CC assay. The ligands that are identified may be used alone or in
 CC combination with the MAFA to prevent inflammatory and allergic reactions

XX SQ Sequence 114 AA;
Query Match 53.5%; Score 551; DB 2; Length 114;
Best Local Similarity 84.1%; Pred. No. 1.9e-51;
Matches 95; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 75 CPILWTRNGSHCYFYSMEKDWNSLKFCADKSGHLLTFPDNQGVKLFGEYLGDFYWG 134
DB 1 CPNLWNRNGSHCYFYSMEKDWNSLKFCADKSGHLLTFPDNQGVNLFQEVGDFYWG 60
QY 135 LRNIDGWRWEGGPPALSRLITNSLIQRCGAIHRNGLOASSCEVALQWICKVL 187
DB 61 LRIDGWRWEDGPPALSRLITNSLVVQKGTTHRCGLHASSCEVALQWICKVL 113
RESULT 6
AAW88267
ID AAW88267 standard; protein; 99 AA.
XX AC AAW88267;
XX DT 29-MAR-1999 (first entry)
XX DE Human MAPA splice variant huMAFA(E3/4-).
XX KW Mast cell function-associated antigen; MAPA; huMAFA(E3/4-);
XX KW splice variant; human; inflammation; allergy; asthma;
XX KW rheumatoid arthritis; tumour; therapy.
XX OS Homo sapiens.
XX PN WO3854209-A2.
XX PD 03-DEC-1998.
XX PF 29-MAY-1998; 98WO-GB001572.
XX PR 31-MAY-1997; 97GB-00011148.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX DR WPI: 1999-059806/05.
XX DR N-PSDB; AAV84200.
XX New polypeptide having a sequence corresponding to human mast cell
function-associated antigen - useful in forming and manufacturing
pharmaceutical compositions in the treatment of inflammatory and allergic
diseases, and tumour growth.
XX Disclosure; Fig 3; 44pp; English.
XX This is the amino acid sequence of human mast cell function- associated
antigen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-
like domain of human MAFA (see AAW88265) but retains the intracellular
and transmembrane domains as well as the extracellular C-terminal tail.
XX Truncated MAFA polypeptides including huMAFA(E3/4-), and polynucleotides
encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-
72), can be used in compositions for the treatment of
XX inflammatory and allergic diseases (e.g. rheumatoid arthritis and
XX asthma), or tumour growth
XX SQ Sequence 99 AA;
Query Match 21.6%; Score 222.5; DB 2; Length 99;
Best Local Similarity 30.1%; Pred. No. 5.9e-16;
Matches 56; Conservative 13; Mismatches 28; Indels 89; Gaps 1;
QY 1 MADSTSYTLELPEAPQVQDESRLKAVLHRLPHSLRFAMVALGLTILVLSLIMYQRL 60
DB 1 MTDVSYLSMLELPTAQONDYGFQKSSSRPSCSLVAIALGLLTVLLSLYQWIL 60

QY 61 CCGSKDSTGCHPSCPILWTRNGSHCYFYSMEKDWNSLKFCADKSGHLLTFPDNQGVK 120
DB 61 CQG----- 63
QY 121 LFGEYLGDFYWGILNRNIDGWRWEGGPPALSRLITNSLIQRCGAIHRNGLOASSCEVALQ 180
DB 64 -----ISSNSFVQTCGAIHRNGLOASSCEVPLH 91
QY 181 WICKKV 186
DB 92 WVCKKV 97
RESULT 7
AAW64791
ID AAW64791 standard; protein; 179 AA.
XX AC AAW64791;
XX DT 23-NOV-1998 (first entry)
XX DE Human Kp43 protein.
XX KW Kp43; human; natural killer cell surface antigen; NK; T cell; inhibitor;
XX KW cell-mediated cytotoxicity; transplant rejection; autoimmune disease.
XX OS Homo sapiens.
XX PN US5811284-A.
XX PD 22-SEP-1998.
XX PF 20-MAY-1996; 96US-00650578.
XX PR 29-DEC-1993; 93US-00175339.
XX PA (SCHE) SCHERING CORP.
XX PA (LOPEZ/) LOPEZ-BOTET M.
XX PA (BELT/) BELTRAN J A.
XX PI Lanier LL, Chang C, Lopez-Botet M, Beltran JA, Phillips JH;
XX DR WPI: 1998-530877/45.
XX DR N-PSDB; AAV46476.
XX DNA encoding natural killer cell surface antigen Kp43 - and transformed
cells for producing recombinant Kp43.
XX Claim 1; Col 31-32; 17pp; English.
XX This sequence represents a novel human natural killer (NK) cell surface
antigen, Kp43. This sequence can be used in a method resulting in the
XX production of recombinant protein expressed by NK and T cells, which may
XX inhibit cell-mediated cytotoxicity, e.g. in transplant rejection or
XX autoimmune diseases, or may be used to produce antibodies for diagnostic
XX or therapeutic use
XX SQ Sequence 179 AA;
Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 7.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLTILVLSLIMYQRLCCGS-----KDSTGCHPSCPILWTRNGS 84
DB 14 GTLIGLICSLMATLGLIKNSFTKLSIRPAFTPGNIELQKSDC--C-SCQEKWGYRC 70
QY 85 HCYFYSMEKDWNSLKFCADKSGHLLTFPDNQGVKLFGEYLGDFYWGILNRNID---GW 141
DB 71 NCYFISSEQKTWNESRHLCAKQSSLLQQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RNEGGPPALSRLITN---SLIQRCGAIHRNG-LOASSCEVALQWICKKV 187

PR 27-SEP-1996; 96US-00721798.

AC AAU19660;

AC AAU19660;

DT 04-DEC-2001 (first entry)
XX Human novel extracellular matrix protein, Seq ID No 310.
DE
XX
XX Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV;
KW antianemic; antirheumatic; antisclerotic; cardiant; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;
KW antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
KW cancers; hyperproliferative disorder; breast neoplasm; melanoma;
KW Sezary syndrome; Gaucher's disease; neurological diseases;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW cardiac arrest; tachycardia; angina; infection; corneal infections;
XX wound healing; immunogen; gene therapy; antisenese; food additive.
XX
OS Homo sapiens.
XX
XX WC200155368-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001348.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190706P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205151P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 01-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
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PR 14-AUG-2000; 2000US-0225214P.
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PR 02-OCT-2000; 2000US-0236370P.
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PR 13-OCT-2000; 2000US-0239335P.
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PR 20-OCT-2000; 2000US-0241808P.
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PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.

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OM protein - protein search, using sw model

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Title: US-09-811-367B-3

Perfect score: 1029

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	178.5	17.3	179	15	US-10-335-009-10
5	160.5	15.6	181	13	US-10-114-893-22
6	156	15.2	182	9	US-09-764-870-310
7	156	15.0	182	14	US-10-125-540-310
8	154	15.0	165	10	US-09-759-130B-98
9	154	15.0	165	16	US-10-741-790-98
10	151	14.7	132	15	US-10-335-009-4
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17	147	14.3	35	9	US-09-864-761-33902	Sequence 33902, A
18	145	14.1	145	10	US-09-759-130B-108	Sequence 108, App
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23	144	14.0	149	13	US-10-114-893-32	Sequence 32, Appl
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36	137	13.3	187	16	US-10-741-790-86	Sequence 86, Appl
37	137	13.3	187	16	US-10-775-640-12	Sequence 12, Appl
38	135	13.1	133	12	US-10-239-656-3	Sequence 3, Appli
39	135	13.1	143	12	US-10-239-656-2	Sequence 2, Appli
40	135	13.1	162	12	US-10-239-656-90	Sequence 90, Appl
41	129.5	12.6	124	12	US-09-964-956-67	Sequence 67, Appl
42	129.5	12.6	124	12	US-10-072-012-836	Sequence 836, App
43	129.5	12.6	158	9	US-09-929-230-11	Sequence 11, Appl
44	129.5	12.6	158	14	US-10-226-420-11	Sequence 11, Appl
45	129	12.5	149	15	US-10-335-009-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takayashi, No. US20020155110A1uaki
; APPLICANT: Makayashi, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-811-367B-3

Query Match	100.0%	Score 1029;	DB 9;	Length 188;
Best Local Similarity	100.0%	Pred. No. 7.9e-101;		
Matches 188;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MADSSYSTLELPEAPQVQDES	SWKLVLRHPLSRFAMVGLGLT	VILMSILMYQRIIL 60
Db	1	MADSSYSTLELPEAPQVQDES	SWKLVLRHPLSRFAMVGLGLT	VILMSILMYQRIIL 60
QY	61	CCGSKDSTCHSCPCILWTRNGSHCYFYSMEKWN	SKLFCADKSGHLLTTPDNGVK 120	
Db	61	CCGSKDSTCHSCPCILWTRNGSHCYFYSMEKWN	SKLFCADKSGHLLTTPDNGVK 120	
QY	121	LFGEYLQDGYFWTGLRNIQGWEGG	PALSRLTLTNSLTCRCGAIHNGLOASSCEVALQ 180	
Db	121	LFGEYLQDGYFWTGLRNIQGWEGG	PALSRLTLTNSLTCRCGAIHNGLOASSCEVALQ 180	


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; FILE REFERENCE: PTZ14C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 310
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-540-310

Query Match      15.2%; Score 156; DB 14; Length 182;
Best Local Similarity 29.2%; Pred.No.3.le-08;
Matches 40; Conservative 18; Mismatches 59; Indels 20; Gaps 6

QY      60 LCCG-SKDTCTCHPCPILWTRNGSHCYFYSMEKKDWNSSLKPCADKGSHLLTFPDNQG 118
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      53 LCASRSADQTV-----LCQSEWLXYQKCYWFSNEMKSWSDSYVYCLERKSHLLIHDQLE 108
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      119 VKLFGYVLGO-DPYWITGLRNI--GWRWEGGPAALSRLI-----TNSLIQRCGAHR 167
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      109 MAFIQKQLQNLQYVWLGILNFTSLKMTWTWVDGSPIDSKIFFIKPAKENS-----CAAIKE 164
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      168 NGLQASSCRVALQWICK 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      165 SKIFSETCSVFKEWICQ 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-759-130B-98
; Sequence 98, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OT
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460

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; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 340
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-340-340

Query Match      14.4%; Score 148.5; DB 14; Length 140;
Best Local Similarity 26.2%; Pred. No. 1.4e-07;
Matches 32; Conservative 23; Mismatches 64; Indels 3; Gaps 3;

Qy 69 CSHCPGSP-CPILWTRNGSHCYFESMEKKDWNSSLKFCADKGSLLLTFFPDNQGVLFGYLG 127
Db 19 CIKCEAPCPEDWLLYGRKCYFFSEPRDWTGROYCHTHEAVLAVIQSQKELEFEMFKETR 78

Qy 128 QDFYWIGLRNI-DGWRWEGGPALSLRLITNSLIQRCGAHENGGLQASCEVALQWICKKV 186
Db 79 RE-FWIGLRRYGDSEHFWNGDPFDDTFTIAGPGCEVFEPTRLVSTECLEMTREPWCCKM 137

Qy 187 LY 188
Db 138 AY 139
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Search completed: August 10, 2004, 16:53:37
Job time : 41.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:40:40 ; Search time 14.5 Seconds
(without alignments)
669.357 Million cell updates/sec

Title: US-09-811-367B-3
Perfect score: 1029
Sequence: 1 MADSSIVTLELPEAPQVQD.....GLQASSCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 303002

Minimum DB seq length: 0
Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	838	81.4	188	3	US-08-722-126A-5
2	838	81.4	188	5	PCT-US95-04258-5
3	551	53.5	114	3	US-08-722-126A-6
4	551	53.5	114	5	PCT-US95-04258-6
5	267	25.9	76	4	US-09-531-056A-23
6	178.5	17.3	179	1	US-08-690-095-9
7	178.5	17.3	179	2	US-08-650-578-2
8	178.5	17.3	179	2	US-08-688-342-3
9	178.5	17.3	179	2	US-09-113-788-3
10	178.5	17.3	179	3	US-09-113-789-9
11	152	14.8	122	3	US-08-722-126A-9
12	152	14.8	122	5	PCT-US95-04258-9
13	150.5	14.6	115	3	US-08-722-126A-8
14	150.5	14.6	115	5	PCT-US95-04258-8
15	146	14.2	135	3	US-08-543-246B-19
16	145	14.1	173	4	US-09-531-056A-4
17	139.5	13.6	176	3	US-08-772-440-8
18	139.5	13.6	180	3	US-08-772-440-31
19	137	13.3	187	4	US-09-127-946-12
20	136.5	13.3	129	3	US-08-722-126A-10
21	136.5	13.3	129	5	PCT-US95-04258-10
22	135	13.1	134	3	US-08-543-246B-20
23	134.5	13.1	126	3	US-08-772-440-10
24	134	13.0	120	3	US-08-543-246B-18
25	134	13.0	135	3	US-08-543-246B-17
26	133.5	13.0	77	4	US-09-531-056A-22
27	132.5	12.9	79	4	US-09-531-056A-19

28 127 12.3 77 4 US-09-531-056A-21
29 127 12.3 78 4 US-09-531-056A-15
30 127 12.3 78 4 US-09-531-056A-16
31 125 12.1 78 4 US-09-531-056A-18
32 124.5 12.1 117 1 US-07-614-443A-2
33 124.5 12.1 117 1 US-08-294-859-2
34 124.5 12.1 117 1 US-08-481-876-2
35 124.5 12.1 123 1 US-07-893-929A-4
36 124.5 12.1 123 5 PCT-US92-10344-4
37 120 11.7 149 4 US-09-489-847-167
38 119 11.6 87 4 US-09-489-847-326
39 119 11.6 107 1 US-07-893-929A-6
40 119 11.6 107 5 PCT-US92-10344-6
41 117.5 11.4 168 3 US-08-772-440-17
42 116 11.3 115 6 5514582-18
43 115 11.2 175 3 US-08-772-440-15
44 114.5 11.1 125 1 US-07-893-929A-3
45 114.5 11.1 125 5 PCT-US92-10344-3

ALIGNMENTS

RESULT 1

US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-5

Query Match 81.4%; Score 838; DB 3; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.8e-86;

[illegible]

RESULT 2
PCT-US95-04258-5
; Sequence 5, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECTHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04258-5

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QY 121 LFEYVIGDDYWTGLRNDIDWRWEGGPAISLILITNSLIQPCGAHHRNGLOASSCEVALQ 181
Db 121 LFEYVIGDDYWTGLRNDIDWRWEGGPAISLILITNSLIQPCGAHHRNGLOASSCEVALQ 181
QY 181 WICKKVL 187
Db 181 WICEKVL 187
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RESULT 3
US-08-722-126A-6
; Sequence 6, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-6

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RESULT 4
PCT-US95-04258-6


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1 TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
2
3 NUMBER OF SEQUENCES: 5
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Incyte Pharmaceuticals, Inc.
6 STREET: 3174 Porter Drive
7 CITY: Palo Alto
8 STATE: CA
9 COUNTRY: US
10 ZIP: 94304
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Diskette
14 COMPUTER: IBM Compatible
15 OPERATING SYSTEM: DOS
16
17 SOFTWARE: FastSeq Version 1.5
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/688,342
20 FILING DATE: Filed Herewith
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Billings, Lucy J.
23 REGISTRATION NUMBER: 36,749
24 REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 415-855-0555
27 TELEFAX: 415-845-4166
28
29 INFORMATION FOR SEQ ID NO: 3:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 179 amino acids
32 TYPE: amino acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: peptide
36 IMMEDIATE SOURCE:
37 LIBRARY: GenBank
38 CLONE: 1098616
39
40 US-08-688-342-3
41
42 Query Match 17.3%; Score 178.5; DB 2; Length 179;
43 Best Local Similarity 31.8%; Pred. No. 3.5e-12; Indels 31; Gaps 7;
44 Matches 54; Conservative 17; Mismatches 68;
45
46 QY 44 GLLTVILMSILMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
47 DB 14 GTGIICLSLMTATIGILLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SCQEKWVG YRC 70
48
49 QY 85 HCYYFMEKKNWNSLKFCADKGSHLLTFPDNGVKLFGEYLQDFYWGRLNID----GW 141
50 DB 71 NCYFISSEQKTWNEHRHLCASQKSSLLQLONTDELDFMSS--SQQFYWIGLSYSEHTAW 128
51
52 QY 142 RWEGGSAISRLILTN---SLIQRCAHNRNG-LQASCEVALQWICKKVL 187
53 DB 129 LWENGSAISQYLPFPSTFTNTKNCIAVNPNGNALDESCEDKNRYICKQQL 178
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55 RESULT 9
56 US-09-113-788-3
57 Sequence 3, Application US/09113788
58 Patent No. 5969104
59 GENERAL INFORMATION:
60 APPLICANT: Au-Young, Janice
61 APPLICANT: Cocks, Benjamin G.
62 APPLICANT: Goli, Surya K.
63 APPLICANT: Hillman, Jennifer L.
64
65 TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
66
67 NUMBER OF SEQUENCES: 5
68 CORRESPONDENCE ADDRESS:
69 ADDRESSEE: Incyte Pharmaceuticals, Inc.
70 STREET: 3174 Porter Drive
71 CITY: Palo Alto
72 STATE: CA
73 COUNTRY: US
74 ZIP: 94304
75
76 COMPUTER READABLE FORM:

```

```

RESULT 7
US-08-650-578-2
; Sequence 2, Application US/08650578
; Patent No. 5811284
; GENERAL INFORMATION:
; APPLICANT: Chang, Chiwen
; APPLICANT: Aramburu Beltran, Jose
; APPLICANT: Lopez-Botet, Miguel
; APPLICANT: Phillips Jr., Joseph H.
; APPLICANT: Lanier, Lewis L.
; TITLE OF INVENTION: Purified Mammalian NK Antigen and
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,578
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,339
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-650-578-2

Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLIMYORILCCGS-----KDSCTSHCPSPILWTRNGS 84
Db 14 GTLGIICLSMATIGILLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SQQRKMWGYRC 70
QY 85 HCYYFSMEKDWNSSLKFCADKGHLITFPDQGVKLFGEVLGQDFWIGLRNID---GW 141
Db 71 NCYFISSEQKTWNEHSRLCAQSQSLSLQLQNTDELDFMSS--SQQFYWIGLSYEHTAW 128
QY 142 RWEGGPALSLRILTN--SLIQRGATHRG-LQASCEVALOWICCKVL 187
Db 129 LWNGSALSQVLFPSFTFNKNCIAYNPNGNALDESCEDKNRYICKQOL 178

RESULT 8
US-08-688-342-3
; Sequence 3, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surva K.

```



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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,788
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/688,342
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
; US-09-113-788-3

Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCPILWTRNGS 84
Db 14 GTLGIIICLSMATIGILLKNSFTKLSIEPAFTPGNIELQKSDC--C-SQCKWVGRC 70

QY 85 HCYVFSMEKKDWNSSLKFCADKGSLLTFFPDNQVKLFGEVLGDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNSRHLCASQKSSLLQLQNTDELFMSS--SQOFYWGISYEHTAW 128

QY 142 RWEGGPALSRLITN---SLIQRGAIHRNG-LQASCEVALQWICKKVL 187
Db 129 LWENGSAISQVLPSPFETFTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 10
US-09-113-789-9
; Sequence 9, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,789
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
; US-09-113-789-9

Query Match 17.3%; Score 178.5; DB 3; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCPILWTRNGS 84
Db 14 GTLGIIICLSMATIGILLKNSFTKLSIEPAFTPGNIELQKSDC--C-SQCKWVGRC 70

QY 85 HCYVFSMEKKDWNSSLKFCADKGSLLTFFPDNQVKLFGEVLGDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNSRHLCASQKSSLLQLQNTDELFMSS--SQOFYWGISYEHTAW 128

QY 142 RWEGGPALSRLITN---SLIQRGAIHRNG-LQASCEVALQWICKKVL 187
Db 129 LWENGSAISQVLPSPFETFTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 11
US-08-722-126A-9
; Sequence 9, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAPA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618

```

REFERENCE/DOCKET NUMBER: PECHT-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-722-126A-9

Query Match 14.8%; Score 152; DB 3; Length 122;
Best Local Similarity 27.9%; Pred. No. 2e-09; Indels 8; Gaps 3;
Matches 34; Conservative 22; Mismatches 58;

QY 75 CPILWTRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTFPPDNOGVKLFGEYLGQDF--YW 132
Db 1 CPQDWLSHRDKCFHVSQVSNWTWEEGLVDCDCKGATMLIQOEELRFLDSIKKYNQSF 60
QY 133 IGLRNI---DQWRWEGGPALS---LRILTNSLIQRCGAHNRGLQASCEVALQWICKV 186
Db 61 IGLRYTLPDMNWKWINGSTLNSDLKGTDTENDSCAAISGDKVTFESCNSDNRWICQKE 120
QY 187 LY 188
Db 121 LY 122

RESULT 12
PCT-US95-04258-9
Sequence 9, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04258-9

Query Match 14.8%; Score 152; DB 5; Length 122;
Best Local Similarity 27.9%; Pred. No. 2e-09; Indels 8; Gaps 3;
Matches 34; Conservative 22; Mismatches 58;

QY 75 CPILWTRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTFPPDNOGVKLFGEYLGQDF--YW 132
Db 1 CPQDWLSHRDKCFHVSQVSNWTWEEGLVDCDCKGATMLIQOEELRFLDSIKKYNQSF 60
QY 133 IGLRNI---DQWRWEGGPALS---LRILTNSLIQRCGAHNRGLQASCEVALQWICKV 186
Db 61 IGLRYTLPDMNWKWINGSTLNSDLKGTDTENDSCAAISGDKVTFESCNSDNRWICQKE 120
QY 187 LY 188
Db 121 LY 122

RESULT 13
US-08-722-126A-8
Sequence 8, Application US/08722126A
Patent No. 6034227
GENERAL INFORMATION:
APPLICANT: PECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: UNITED STATES OF AMERICA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-722-126A-8

Query Match 14.6%; Score 150.5; DB 3; Length 115;
Best Local Similarity 26.3%; Pred. No. 2.8e-09; Indels 5; Gaps 3;
Matches 30; Conservative 20; Mismatches 59;

QY 75 CPILWTRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTFPPDNOGVKLFGEYLGQDFYWG 134
Db 1 CSEDWVGYQKCYFISTVTKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHWG 60

```
QY 135 LRNIDG--WRWEGGPALSLRI-LTNSLIQRCGAHNRGLQASCEVALQWICKK 185
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 LKKEPGHPKWSNGKEFNWPNVTGS--DKCVFLKNTVSSMECEKNLYWICNK 112
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
PCT-US95-04258-8
; Sequence 8, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IEM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04258-8

Query Match 14.6%; Score 150.5; DB 5; Length 115;
Best Local Similarity 26.3%; Pred. No. 2.0e-09;
Matches 30; Conservative 20; Mismatches 59; Indels 5; Gaps 3;

QY 75 CPILWTRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTTPDNQGVKLFGEYLQDFFWIG 134
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 CSEDWVGYQKCYFISTVKESWTSQAQACSEHGATLAVIDSEKDMFLKEYAGREHWG 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 135 LRNIDG--WRWEGGPALSLRI-LTNSLIQRCGAHNRGLQASCEVALQWICKK 185
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 LKKEPGHPKWSNGKEFNWPNVTGS--DKCVFLKNTVSSMECEKNLYWICNK 112
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-08-543-246B-19
; Sequence 19, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
```

```
; ADDRESSEE: No. 6262244artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IEM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kasenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; US-08-543-246B-19

Query Match 14.2%; Score 146; DB 3; Length 135;
Best Local Similarity 28.9%; Pred. No. 1.1e-08;
Matches 35; Conservative 18; Mismatches 62; Indels 6; Gaps 4;

QY 71 HCPSCPILWTRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTTPDNQGVKLFGEYLQDFF 130
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 17 HCGHCPPEWITYSNCSYIGKERTWEESLLACTSKNSLLSIDNEEIKFLASILPSS- 75
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 131 YWTGL-RNIDGWRWE--GGPALSLRIITNSLIQ-RCGAHNRGLQASCEVALQWICKKY 186
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 -WIGVFRNSSHPWVTINGLAFKHKIKSDNAELNCVLQVNLKSAQCSSMIYHCKHK 134
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 187 L 187
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 135 L 135
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: August 10, 2004, 16:45:20
Job time : 15.5 secs
```

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:39:40 ; Search time 13.5 Seconds
(without alignments)
1339.556 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSTLELPAPRVQD.....GLHASSCEVALQWICEKVLP 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 95185

Minimum DB seq length: 0
Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2 I59421	mast cell function
2	162.5	15.7	170	2 T28140	natural killer cell
3	158	15.3	156	2 T28141	C type lectin, B 1
4	146	14.1	146	2 JC7135	agkisactucin beta
5	137	13.2	167	1 WMVZF2	hepatic lectin hom
6	134.5	13.0	144	2 PC7027	aggrelin alpha cha
7	127.5	12.3	146	2 JC4691	coagulation factor
8	126	12.2	133	2 A47267	botroctetin alpha c
9	123.5	11.9	125	2 B47267	botroctetin beta ch
10	121.5	11.7	146	2 JC7105	aggrelin beta chai
11	115	11.1	123	2 B42972	coagulation factor
12	114.5	11.1	152	2 JC7134	agkisactucin alph
13	113	10.9	116	1 WMVZF8	hepatic lectin hom
14	112.5	10.9	162	1 LNRC3	lectin BRA3-2 prec
15	112	10.8	162	1 LNRC1	perlucin - Halioti
16	108.5	10.5	155	2 S78774	pancreatitits-assoc
17	103.5	10.0	175	2 A49616	coagulation factor
18	102.5	9.9	129	2 JC4329	regenerating islet
19	102	9.8	166	1 RGHU1A	pancreatic stone p
20	102	9.8	166	2 A45751	bitiscetin beta ch
21	100.5	9.7	125	2 JC5059	lectin, galactose-
22	100	9.7	135	2 A38609	pancreatic stone p
23	98	9.5	165	2 A28351	echicetin beta cha
24	96.5	9.3	123	2 JC2415	coagulation factor
25	96.5	9.3	122	2 JC4690	regenerating islet
26	95	9.2	166	1 RGHU1B	pancreatitits-assoc
27	94.5	9.1	175	2 S29822	reg II, regenerati
28	94	9.1	173	2 B47148	pancreatitits-assoc
29	92.5	8.9	174	2 S54979	

30 92 8.9 175 2 A41719 pancreatic stone p
31 91 8.8 163 1 A34313 antifreeze protein
32 89.5 8.6 131 2 JC5058 bitiscetin alpha c
33 88 8.5 175 2 A37194 pancreatic thread
34 87 8.4 147 2 JC7938 type II antifreeze
35 87 8.4 153 2 T21396 hypothetical prote
36 87 8.4 173 2 SI0548 lectin - barnacle
37 86 8.3 40 2 S56007 echinoidin - sea c
38 85 8.2 147 2 A26697 reg I, regeneratin
39 82 7.9 165 2 A47148 antifreeze protein
40 82 7.9 175 1 JH0626 ovocleidin - chick
41 81.5 7.9 142 2 S78596 hepatic lectin hom
42 81.5 7.9 143 1 WMVZEL regenerating prote
43 79 7.6 174 2 I83377 hypothetical prote
44 78.5 7.6 166 2 T28809 alboaagreglin-B alp
45 77 7.4 40 2 B56829

ALIGNMENTS

RESULT 1
I59421
mast cell function associated antigen - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I59421
R;Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A;Title: A secretion inhibitory signal transduction molecule on mast cells is another ()
A;Reference number: I59421; MUID:96016176; PMID:7568140
A;Accession: I59421
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-188 <RES>
A;Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C;Genetics:
A;Gene: mafa

Query Match 100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.2e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAPRVQDSSRWKVKAVLHRCPCVSYLVNVALGLLTVILMSLLLYQRTL 60
Db 1 MADNSIYSTLELPAPRVQDSSRWKVKAVLHRCPCVSYLVNVALGLLTVILMSLLLYQRTL 60
QY 61 CCGSKGFMCSQCSRCPCNLWMRNGSHCYFMSMEKEDWNSSLKFCADKSGHLLTFPDNQGYN 120
Db 61 CCGSKGFMCSQCSRCPCNLWMRNGSHCYFMSMEKEDWNSSLKFCADKSGHLLTFPDNQGYN 120
QY 121 LFOEYVGEDFYWTIGLRDIDGWRWEDGPALSLSLTSLNSVQKCGTIHRCGLHASSCEVALQ 180
Db 121 LFOEYVGEDFYWTIGLRDIDGWRWEDGPALSLSLTSLNSVQKCGTIHRCGLHASSCEVALQ 180
QY 181 WICEKVLP 188
Db 181 WICEKVLP 188

RESULT 2
T28140
natural killer cell receptor homolog - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28140
R;Milne, S.; Kaufman, J.; Beck, S.
Submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility comp
A;Reference number: Z20475
A;Accession: T28140
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA

A;Residues: 1-170 <MIL>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAA18960.1
A;Experimental source: clone cB12
C;Genetics:
A;Gene: B-NK
A;Map position: 16
A;Note: Intron positions not resolved (incomplete sequence)

Query Match 15.7%; Score 162.5; DB 2; Length 170;
Best Local Similarity 28.1%; Pred. No. 4.8e-08;
Matches 34; Conservative 16; Mismatches 60; Indels 11; Gaps 3;

QY 72 CSRCPNLMWRNGSHCYFSEMEKRDWNSSLKPCADKGGSHLLTFPDNQGNLFQYVGGDFY 131
DB 47 CLLCPQFWRLLGDRCYELSTKGNWTQAKKCNLQSLAVLRKKAEDHLQWAGAEVP 106
QY 132 WIGLR-DIDGWRWEDGPAL-----SLILSNVSVQKGTTHRCGLHASSCEVALQWICE 184
DB 107 WIGLEVSTNQKWDNSNSYNSTESDNLVSMEN---RCGTFKTKVEGDVCSGEHQWVCQ 162
QY 185 K 185
DB 163 K 163

RESULT 3
T28141
C type lectin, B locus - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28141
R;Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex
A;Reference number: Z20475
A;Accession: T28141
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-156 <MIL>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1
A;Experimental source: clone cB12
C;Genetics:
A;Gene: BLEC
A;Map position: 16
A;Introns: 17/1; 74/3; 110/2

Query Match 15.3%; Score 158; DB 2; Length 156;
Best Local Similarity 27.5%; Pred. No. 1.2e-07;
Matches 33; Conservative 22; Mismatches 55; Indels 10; Gaps 4;

QY 72 CSRCPNLMWRNGSHCYFSEMEKRDWNSSLKPCADKGGSHLLTFPDNQGNLFQYVGGDFY 131
DB 27 CAQCQPFDMGFRGKCYFSEDSNWTSSQNNCSALGASLAVFDSAEILSFTWRHKGSSPH 86
QY 132 WIGLRDIDG---WRWEDGPALS--LSILSNVSVQKGTTHRCGLHASSCEVALQWICEK 185
DB 87 WVGL-SREGKEHPWENVRNPSLHFLVQGDGL---CAYLGDAGLSSSHCSSTRNWNVCTK 142

RESULT 4
JC7135
agkisacutacin beta chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenlytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7135; PC7038
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7135
A;Molecule type: mRNA
A;Residues: 1-146 <CHE>

A;Cross-references: GB:AF176421
A;Experimental source: venom gland
A;Accession: PC7038
A;Molecule type: protein
C;Residues: 24-50;59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: agkisacutacin beta chain #status experimental <MAT>

Query Match 14.1%; Score 146; DB 2; Length 146;
Best Local Similarity 27.7%; Pred. No. 1.5e-06;
Matches 41; Conservative 19; Mismatches 50; Indels 38; Gaps 6;

QY 39 VMVALGELLTVILMSLLYQRTLCGSGKGFMCSCQSRCPNLMWRNGSHCYFSEMEKRDWNS 98
DB 5 IFVSFGLLVFLS-----LSGTAAADCPSEWSSVEGHCYKPFDFEKTWAD 48
QY 99 SLKFCAD--KGSHLLTFPDNQG---VNLFOEYVGGDFYWIGLRDI-DG--WRWEDGPAL 149
DB 49 AEKFTQKHGKSHLASFHSSEADFVVTLTPTPSLTKDLVWIGLKNWNGCYKRWSDGTKL 108
QY 150 -----SLILSNVSVQKCGT 164
DB 109 DYKDWREQFECLVSRVTNNWNLMSMDCGT 136

RESULT 5
WMVZF2
hepatic lectin homolog (BamHI-ORF2) - fowlpox virus (isolate HP-438 [Munich])
C;Species: fowlpox virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Accession: B29963
R;Tomley, P.; Binns, M.; Campbell, J.; Boursnell, M.
J. Gen. Virol. 69, 1025-1040, 1988
A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox
A;Reference number: JT0442; MUID:88229622; PMID:2836548
A;Accession: B29963
A;Molecule type: DNA
A;Residues: 1-167 <TOM>
A;Cross-references: GB:D00295; NID:g221380; PIDN:BAA00192.1; PID:g221383
C;Superfamily: fowlpox virus hepatic lectin homolog; C-type lectin homology
C;Keywords: early protein
F;49-152/Domain: C-type lectin homology <LCH>

Query Match 13.2%; Score 137; DB 1; Length 167;
Best Local Similarity 29.1%; Pred. No. 1.2e-05;
Matches 44; Conservative 21; Mismatches 78; Indels 8; Gaps 4;

QY 35 VSYLVVMVALGLTLVILMSLLYQRTLCGSGKGFMCSCQSRCPNLMWRNGSHCYFSEMEKR 94
DB 12 VSCYAITVLGILCLILFTLV---VVTCKVYVAFYFYSKVCPEDEWIGYNSKCYFTINET 68
QY 95 DWSLSLKFCADKGGSHLLTFPDNQGNLFQYVGGDFYWIGLRDIDGWEDGPALSIL 154
DB 69 NWNDSKGLCDWMSLIRFDNIETLNFVSRV-GKGSYWI---DINQNRKIPGINFSL-YY 123
QY 155 SNSVSVQKCGTTHRCGLHASSCEVALQWICEK 185
DB 124 EQVNDICLLPFTSNIEWSCIHFHRTICVK 154

RESULT 6
PC7027
aggreitin alpha chain - Malayan pit viper (fragment)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C;Accession: PC7027
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggreitin, a collagen-like platelet
A;Reference number: PC7027; MUID:99443731; PMID:10512747
A;Accession: PC7027

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:36:04 ; Search time 8 seconds

(without alignments)
1223.649 Million cell updates/sec

Title: US-09-811-367b-5

Perfect score: 1036

Sequence: 1 MADNSIYSTLELPAARVQD.....GLHASCEVALQWICEKVLIP 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 40997

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163.5	15.8	179	1	Q9mzk9 macaca mula
2	155	15.0	179	1	Q13241 homo sapien
3	155	15.0	179	1	Q9mz41 pan troglod
4	154	14.9	163	1	P14371 fowlpox vir
5	153.5	14.8	149	1	C1E22_HUMAN
6	148.5	14.3	133	1	RHCA_AGRH
7	140.5	13.6	148	1	CVXB_CRODU
8	137	13.2	167	1	V008_FOWPV
9	132.5	12.8	117	1	CHBB_CROHO
10	131	12.6	157	1	MMHB_AGKHA
11	130	12.5	146	1	MMHB_AGKHA
12	127.5	12.3	146	1	IXB_TRIFL
13	126	12.2	133	1	B0T4_BOTJA
14	124.5	12.0	123	1	ABA4_TRIAB
15	123.5	11.9	125	1	B0T6_BOTJA
16	113	10.9	162	1	LEC3_MGRO
17	111.5	10.8	158	1	CVXA_CRODU
18	109.5	10.6	125	1	ABA4_TRIAB
19	109.5	10.6	155	1	PLC_HALLA
20	107.5	10.4	129	1	RHCB_AGRH
21	106.5	10.3	118	1	ABBB_TRIAB
22	103.5	10.0	131	1	ABAI_TRIAB
23	103.5	10.0	175	1	PAP1_HUMAN
24	103	9.9	174	1	PAP3_MOUSE
25	102	9.8	166	1	LITA_HUMAN
26	101.5	9.8	133	1	ECHA_ECHCA
27	100	9.7	135	1	LECG_CROAT
28	99.5	9.6	134	1	ABA2_TRIAB
29	98	9.5	158	1	NGKF_PANTR
30	98	9.5	165	1	LITH_RAT
31	97	9.4	158	1	NGKF_HUMAN
32	96.5	9.3	123	1	ECBH_ECHCA
33	96.5	9.3	152	1	IXA_TRIFL

34	95	9.2	135	1	LECG_LACST
35	95	9.2	166	1	LITB_HUMAN
36	94.5	9.1	175	1	PAP1_MOUSE
37	94	9.1	173	1	LIT2_MOUSE
38	93	9.0	135	1	LECG_BITAR
39	92.5	8.9	158	1	LECG_TRIST
40	92.5	8.9	174	1	PAP3_RAT
41	92	8.9	173	1	LEC2_MGRO
42	92	8.9	175	1	PAP1_RAT
43	91.5	8.8	175	1	PAP2_MOUSE
44	91	8.8	163	1	ANP_HEMAM
45	89.5	8.6	132	1	ABB3_TRIAB

ALIGNMENTS

RESULT 1

CD94_MACMU STANDARD; PRT; 179 AA.

AC Q9Mzk9; Q9GK91; Q9Mzk7; Q9Mzk8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
 DE lectin-like receptor subfamily D, member 1).
 GN KLRD1 OR CD94.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE-20322487; PubMed-10866118;
 RA LaBonte M.L., Levy D.B., Letvin N.L.;
 RT "Characterization of rhesus monkey CD94/NKG2 family members and
 RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,
 and D.";
 RL Immunogenetics 51:496-499(2000).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE-21158386; PubMed-11261935;
 RA Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
 RT "Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative
 RT splicing of 5' exons in rhesus monkey decidua.";
 RL Immunogenetics 53:69-73(2001).
 CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
 CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
 CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
 CC members.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=CD94-A;
 CC IsoId=Q9Mzk9-1; Sequence=Displayed;
 CC Name=2; Synonyms=CD94-B;
 CC IsoId=Q9Mzk9-2; Sequence=VSP_003055;
 CC Name=3; Synonyms=CD94 alt;
 CC IsoId=Q9Mzk9-3; Sequence=VSP_003054;
 CC -!- TISSUE SPECIFICITY: Natural killer cells.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC -----
 CC EMBL; AF190931; AAF74527.1; -;
 CC EMBL; AF190932; AAF74528.1; -;

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DR EMBL; AF190933; AAF74529.1; -
DR EMBL; AF294886; AAG34498.1; -
DR HSP; P22897; IEGG.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00441; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; Polymorphism.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 1 34 MAVFTTLWRISGTLGILGLISLMTGLILKNS -> MAA
(in isoform 3).
FT VARSPLIC 105 105 /FTID=VSP_003054.
FT VARIANT 139 139 L -> LQ (in isoform 2).
FT SEQUENCE 179 AA; 20607 MW; 06212B4494527F07 CRC64;
Query Match 15.8%; Score 163.5; DB 1; Length 179;
Best Local Similarity 31.2%; Pred. No. 4.7e-09;
Matches 39; Conservative 19; Mismatches 58; Indels 9; Gaps 4;
QY 70 SQSRRCPNLRNGSHCYFMERKDWNSLKFCAKDGKSHLLTPDNGVNLFOEYVCE 129
Db 56 SDCCSCHEKGYRCYCFISEEKTNWSEHFCASQKSLQLQNDLDFMSS--SQH 113
QY 130 FYWIGL---RIDGWRWDGPAISLSLSNSVVOQ---CGTHRCG-LHASSCEVALQWI 182
Db 114 FYWIGLSVEHTAWLNGSALSQYLPFPSTFKPKNCIAYNSKGNALDESCETKNRYI 173
QY 183 CEKVL 187
Db 174 CKQQL 178
RESULT 2
CD94 HUMAN
ID CD94 HUMAN STANDARD; PRT; 179 AA.
AC Q13241; Q43321; Q43773; Q9UEB3; Q9UEQ0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1) (KP43).
GN KLRL1 OR CD94.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=96011848; PubMed=7589107;
RA Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
RA Lanier L.L.;
RT "Molecular characterization of human CD94: a type II membrane
RT glycoprotein related to the C-type lectin superfamily.";
RL Eur. J. Immunol. 25:2433-2437(1995).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RX MEDLINE=98139529; PubMed=9472066;
RA Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,

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RA Leirach H., Francis F., Lopez-Botet M.;
RT "Structure of the human CD94 C-Type lectin gene.";
RL Immunogenetics 47:305-309(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Blasoni R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=98267245; PubMed=9601951;
RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,
RA Tohma S., Inoue T., Yamamoto K., Juji T.;
RT "A alternatively spliced form of the human CD94 gene.";
RN Immunogenetics 48:87-88(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q13241-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q13241-2; Sequence=VSP_003053;
CC Name=3; Synonyms=CD94 alt;
CC IsoId=Q13241-3; Sequence=VSP_003052;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PROW; NOTED=CD guide CD94 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd94.htm".
CC -----
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CC -----
DR EMBL; U30610; AAC50291.1; -
DR EMBL; Y14287; CAA74663.1; -
DR EMBL; Y14288; CAA74663.1; JOINED.
DR EMBL; AJ000673; CAA04230.1; -
DR EMBL; AJ000001; CAA03845.1; -
DR EMBL; AB009597; BAA24450.1; -
DR EMBL; AB010084; BAA24451.1; -
DR EMBL; BC028009; AAB28009.1; -
DR PDB; 1B6E; 15-JUN-99.

```


DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative C-type lectin protein FPV239 (BamHI-ORF8).
 GN FPV239.
 OS Fowlpox virus (FPV).
 OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Avipoxvirus.
 OC NCBI_TaxID=10261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20193820; PubMed=10729156;
 RX Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
 RT "The genome of fowlpox virus.";
 RL J. Virol. 74:3815-3831(2000).
 RL [2]
 RP SEQUENCE OF 1-116 FROM N.A.
 RC STRAIN=FP-9 / Isolate HP-438;
 RX MEDLINE=88229622; PubMed=2836548;
 RX Tomley F., Binns M., Campbell J., Boursnell M.E.G.;
 RT "Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
 of fowlpox virus.";
 RL J. Gen. Virol. 69:1025-1040(1988).
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC EMBL; AF198100; AAF44583.1; --
 DR EMBL; D00295; BAA0203.1; --
 DR PIR; R29963; WMVZF8.
 DR HSSP; P05140; 2AFP.
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 KW Hypothetical protein; Lectin.
 FT DOMAIN 48 159 C-TYPE LECTIN.
 SQ SEQUENCE 163 AA; 18635 MW; 5156DC892885532 CRC64;
 Query Match 14.9%; Score 154; DB 1; Length 163;
 Best Local Similarity 22.9%; Pred. No. 3.7e-08;
 Matches 38; Conservative 31; Mismatches 65; Indels 32; Gaps 5;
 QY 33 PCVSLVNVVALGLTLTVILMS-----LLYQRTLCGSGKFMCSQSRCPNLMWRNGS 84
 DB 18 PGCS--IIIVLSVFVILSTRPVPPDIKILY-----CKEGWVGYNK 57
 QY 85 HCYPFMBKRDWNSLKFCAKGSHELLFPDQGNVLFQYVGEDFYWIGLRDID---GW 141
 DB 58 NCYFFSEKNNKSLAVERCKMDQGLTSSKEEFKFLRYKPGNHNWIKGVDFNGTW 117
 QY 142 RWEDGPALSLTSLNSVQKCTIHRGCLHASSCEVALQWCEKVL 187
 DB 118 KLEDGSSYD-NIVPIKIGDCAYLSDRSIMSFCFLPKKWCIRIIL 162
 RESULT 5
 CLE2 HUMAN
 ID CLE2 HUMAN STANDARD; PRT; 149 AA.
 AC Q92478; Q9BS74; Q9UB4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE C-type lectin superfamily member 2 (Activation-induced C-type lectin).
 GN CLEC3F2 OR AICL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97190245; PubMed=9038101;
 RX Hamann J., Montgomery K.T., Lau S., Kucherlapati R., van Lier R.A.W.;
 RT "AICL, a new activation induced antigen encoded by the human NK gene
 complex.";
 RL Immunogenetics 45:295-300(1997).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=10072769;
 RX Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.;
 RT "Selection of cDNAs encoding putative type II membrane proteins on the
 cell surface from a human full-length cDNA bank.";
 RL Gene 228:161-167(1999).
 RL [3]
 RP SEQUENCE FROM N.A.
 TISSUE=Urinary bladder;
 RX MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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 Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
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 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Expressed preferentially in lymphoid tissues,
 and in most hematopoietic cell types.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC EMBL; X96719; CAA65480.1; --
 DR EMBL; AB015628; BAA76495.1; --
 DR EMBL; BC005254; AAO05254.1; --
 DR Genbank; HGNC:2053; CLECSF2.
 DR MIM; 603242; --
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0005530; P: lectin; TAS.
 DR GO; GO:0006960; P: antimicrobial humoral response (sensu Inver. . .; TAS.
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 KW Glycoprotein; Transmembrane; Lectin; signal-anchor.
 FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 8 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 FT DOMAIN 26 149 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 42 145 C-TYPE LECTIN.
 FT DISULFID 46 BY SIMILARITY.

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FT DISULFID 87 144 BY SIMILARITY.
FT DISULFID 123 136 BY SIMILARITY.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 79 79 M -> T (IN REF. 3).
FT CONFLICT 107 107 D -> H (IN REF. 1).
SQ SEQUENCE 149 AA; 17307 MW; 0B4FED23424F6C55 CRC64;

Query Match 14.8%; Score 153.5; DB 1; Length 149;
Best Local Similarity 27.0%; Pred. No. 3.7e-08;
Matches 43; Conservative 27; Mismatches 68; Indels 21; Gaps 6;

QY 31 HRPVSVL-VVVALGLLTILMSLLYLQRTLCCKSGKFCMCSQGRCPNLMWRNGSHCYF 89
Db 5 HKKCFIIVGLVITNTIITLV-----KLTDSQ-SLCPYDWIGFQNKCYF 49

QY 90 SMEKRDWNSLKFCADKSGSHLLTFPDNQGNVLQFQYVGEDFYWIGLRDIDG--WRWEDGP 147
Db 50 SKEEGDWNSKYNCSIQHADLTIIDNLEENFLRYKCSSDHWGLKMAKNRTGQWVDGA 109

QY 148 ALSLSI-LSNSVVQKGTTHRCGLGHASSCEVALQWICEK 185
Db 110 TTFKSGMRGS--EGCAVLSDDGAATVRCYTERKWKICK 146

RESULT 6
RHCA_AGRH STANDARD; PRT; 133 AA.
ID RHCA_AGRH AC P81397;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Rhodocetin alpha subunit.
OS Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Calloselasma.
OX NCBI_TaxID=8717;
RN [1]
RP SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RA Wang R., Kini R.M., Chung M.C.M.;
RT "Rhodocetin, a novel platelet aggregation inhibitor from the venom of
RT Calloselasma rhodostoma (Malayan pit viper): synergistic and
RT noncovalent interaction between its subunits.";
RL Biochemistry 38:7594-7593(1999).
CC -1- FUNCTION: A potent inhibitor of collagen-induced platelet
CC aggregation. Individually, neither subunit inhibits platelet
CC aggregation. Both subunits are essential.
CC -1- SUBUNIT: Heterodimer of one alpha and one beta subunit held
CC together by noncovalent interactions rather than by intersubunit
CC disulfide bridges.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=15955.90; MW ERR=1.44; METHOD=Electrospray.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23806; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Glycoprotein; Signal.
FT CHAIN 1 23 CONVULXIN BETA.
FT DOMAIN 24 148 C-TYPE LECTIN.
FT DISULFID 26 26 INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
(POTENTIAL).
FT DISULFID 27 38 BY SIMILARITY.
FT DISULFID 55 144 BY SIMILARITY.
FT DISULFID 100 100 INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
(POTENTIAL).
FT DISULFID 121 136 BY SIMILARITY.
SQ SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;

Query Match 14.3%; Score 148.5; DB 1; Length 133;
Best Local Similarity 30.3%; Pred. No. 1e-07;
Matches 40; Conservative 27; Mismatches 46; Indels 19; Gaps 7;

QY 75 CPNLWRNGSHCYFSEMEKRDWNSLKPCA--DKGSHLLTFPDNQGNVLQFQYVGEDFY- 131
Db 2 CPDGSNSTSKSYCYRPFPEKKTWEAEARFCTEQEKAHLVSM--ENRLEAVFVDMVMENNFE 60

QY 132 -----WIGLR-DIDGWR-----WEDGPALSLSLTSSNVVQKCGTI--HRCGL--HASSCE 176
Db 61 NKIYRSWIGLTKENQORSNLEWSDGSSISYENLYEPYMEKFCFLMDHQSLPKWHTADCE 120

QY 177 VALQWICEKVLK 188
Db 121 EKNVFMCKQLP 132

RESULT 7
CVXB_CRODU STANDARD; PRT; 148 AA.
ID CVXB_CRODU AC O93437;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Convulxin beta precursor (CVX beta).
OS Convulxin durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
RC TISSUE=Venom gland;
RX MEDLINE=98324901; PubMed=9657980;
RA Leduc M., Bon C.;
RT "Cloning of subunits of convulxin, a collagen-like platelet-
RT aggregating protein from Crotalus durissus terrificus venom.";
RL Biochem. J. 333:389-393(1998).
CC -1- FUNCTION: Binds to the platelet and collagen receptor,
CC glycoprotein VI (GPVI).
CC -1- SUBUNIT: Heterohexamer of three alpha chains and three beta
CC chains; disulfide-linked.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y16349; CAA76182.1; --
DR HSP; P23807; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Glycoprotein; Signal.
FT CHAIN 1 23 CONVULXIN BETA.
FT DOMAIN 24 148 C-TYPE LECTIN.
FT DISULFID 26 26 INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
(POTENTIAL).
FT DISULFID 27 38 BY SIMILARITY.
FT DISULFID 55 144 BY SIMILARITY.
FT DISULFID 100 100 INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
(POTENTIAL).
FT DISULFID 121 136 BY SIMILARITY.
SQ SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;

Query Match 13.6%; Score 140.5; DB 1; Length 148;
Best Local Similarity 29.1%; Pred. No. 7.1e-07;

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:39:05 ; Search time 32 Seconds
(without alignments)
1853.669 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSTLELPAARVQD.....GLHASCEVALQWICEKVLP 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 396094

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	11	Q64335
2	838	80.9	188	11	O88713
3	178	17.2	181	4	Q9NZS1
4	175	16.9	179	11	O54708
5	175	16.9	179	11	O54707
6	173	16.7	165	11	Q9R007
7	171	16.5	165	6	Q9GLF4
8	165.5	16.0	164	11	Q8BL24
9	165	15.9	161	6	Q95JG4
10	161.5	15.8	185	6	Q9GLF3
11	161.5	15.6	179	6	Q8MUY8
12	160	15.4	154	4	Q8WUP7
13	160	15.4	159	6	Q8SPX0
14	159.5	15.4	188	4	Q9NY25
15	158.5	15.3	179	6	Q8MJ13
16	158.5	15.3	179	11	O35778

17	158	15.3	185	6	Q9MZJ6	Q9mzj6 macaca mula
18	157.5	15.2	132	11	Q8R4K5	Q8r4k5 rattus norv
19	157.5	15.2	180	12	Q9DL58	Q9dl58 rat cytoMeg
20	155.5	15.0	179	6	Q8MHY9	Q8mhy9 pongo pygma
21	155	15.0	178	11	Q91ZW9	Q91zw9 mus musculu
22	153	14.8	187	4	Q9UKQ0	Q9ukq0 homo sapien
23	152.5	14.7	179	6	Q8MJ14	Q8mj14 pongo pygma
24	150	14.5	146	13	Q8AYA4	Q8aya4 agkistrodon
25	149.5	14.4	168	11	Q9JKF2	Q9jkf2 mus musculu
26	148	14.3	173	4	Q9HD37	Q9hd37 homo sapien
27	146	14.1	146	13	Q8JIW1	Q8jiw1 agkistrodon
28	145	14.0	146	13	Q9IAM0	Q9iam0 agkistrodon
29	144	13.9	168	4	Q96FA7	Q96pa7 homo sapien
30	143	13.8	148	13	Q8AV98	Q8av98 trimeresuru
31	142	13.7	142	11	Q8CJ86	Q8cj86 mus musculu
32	142	13.7	158	11	Q8OZ35	Q8oz35 mus musculu
33	142	13.7	175	11	Q9JKF3	Q9jkf3 mus musculu
34	142	13.7	183	13	Q8OZS7	Q8ozs7 gallus gall
35	141	13.6	142	11	Q8BHK7	Q8bhk7 mus musculu
36	141	13.6	163	6	Q9GK90	Q9gk90 macaca mula
37	137	13.2	183	6	Q95J54	Q95j54 pan troglod
38	135.5	13.1	146	13	Q8JGT6	Q8jgt6 trimeresuru
39	135.5	13.1	158	13	Q8UVC6	Q8uvc6 agkistrodon
40	135.5	13.1	158	13	Q8AYA5	Q8aya5 agkistrodon
41	134.5	13.0	136	13	Q91841	Q91841 agkistrodon
42	134.5	13.0	146	13	Q7T045	Q7t045 vipera lebe
43	134	12.9	182	11	Q61972	Q61972 mus musculu
44	132.5	12.8	162	6	Q8MJH4	Q8mjh4 pongo pygma
45	132	12.7	164	11	Q9EP94	Q9ep94 mus musculu

ALIGNMENTS

RESULT 1

Q64335 ID Q64335 PRELIMINARY; PRT; 188 AA.
AC Q64335;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MAFA protein.
DE MAFA.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=Testis;
RA Bocek Jr P., Guthmann M.D., Pecht I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016176; PubMed=7568140;
RA Guthmann M.D., Tal M., Pecht I.;
RT "A secretion inhibitory signal transduction molecule on mast cells is
another C-type lectin."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL; X97191; CAA65829.1; JOINED.
DR EMBL; X97192; CAA65829.1; JOINED.
DR EMBL; X97193; CAA65829.1; JOINED.
DR EMBL; X97194; CAA65829.1; JOINED.
DR EMBL; X97195; CAA65829.1; JOINED.
DR EMBL; X79812; CAA56208.1; JOINED.
DR PIR; I59421; I59421.
DR GO; GO:0005529; F.sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT. 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 188 AA; 21356 MW; 2CC8032D4D020B15 CRC64;

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Query Match      100.0%; Score 1036; DB 11; Length 188;
Best Local Similarity 100.0%; Pred. No. 1e-102;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60
Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60

Qy 61 CCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKDWNSSLKFCADKGSLLHLLTFPDNQGWN 120
Db 61 CCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKDWNSSLKFCADKGSLLHLLTFPDNQGWN 120

Qy 121 LFOEYVGEDFWIGLRIDGWRWEDGPAISLSILSNSVVOKGTIHRGCLHASCEVALQ 180
Db 121 LFOEYVGEDFWIGLRIDGWRWEDGPAISLSILSNSVVOKGTIHRGCLHASCEVALQ 180

Qy 181 WICEKVL 188
Db 181 WICEKVL 188

RESULT 2
O88713 PRELIMINARY; PRT; 188 AA.
AC O88713
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-AUG-1999 (TREMBlrel. 11, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-
DE like receptor Gl).
GN KLRG1 OR MAFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17 SCID;
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat '2F1', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
RN [2]
RP SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvevTACfBr; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=11220622;
RA Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor Gl gene (KLRG1), the mouse homologue
RT of MAFA";
RL Immunogenetics 52:206-211(2001).
DR EMBL; AF097357; AAD03718.1; -.
DR EMBL; AF010751; CAA09342.1; -.
DR EMBL; AF317727; AAK40082.1; -.
DR MGB; MGI:1355294; Klrp1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EAL134F1 CRC64;

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Query Match      80.9%; Score 838; DB 11; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.6e-81;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

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Qy 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60
Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60

Qy 61 CCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKDWNSSLKFCADKGSLLHLLTFPDNQGWN 120
Db 61 CCGSKDGTCHPCPILWTRNGSHCYFYSMEKDWNSSLKFCADKGSLLHLLTFPDNQGKV 120

Qy 121 LFOEYVGEDFWIGLRIDGWRWEDGPAISLSILSNSVVOKGTIHRGCLHASCEVALQ 180
Db 121 LFGYLQODFWYIGLRIDGWRWEGGPAISLRILNTSLIQCGAIHRNGLOASCEVALQ 180

Qy 181 WICEKVL 187
Db 181 WICEKVL 187

RESULT 3
Q9NZS1 PRELIMINARY; PRT; 181 AA.
AC Q9NZS1
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Lectin-like receptor F1, splice variant 1 KLRF1-sl.
GN KLRF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KLRF1, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
DR EMBL; AF175207; AAF37805.1; -.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CAB1E551 CRC64;

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Query Match      17.2%; Score 178; DB 4; Length 181;
Best Local Similarity 25.0%; Pred. No. 6.2e-11;
Matches 51; Conservative 32; Mismatches 77; Indels 44; Gaps 9;

Qy 1 MADNSIYSTLELPAAPRVQ--DDSRWKV---AVLHRPCVSYLVMMVAL-----GLTVIIM 51
Db 1 MDQERYMTLVNQSKRSSAQTSLTPKDYSVTLH---WYKILGISGTWNGILTLI 56

Qy 52 SLLLYQRTLCCGSKGFMCSCQRCPNLWMRNGSHCYFYSMEKDWNSSLKFCADKGSLL 111
Db 57 SLIL-----LVLQSEWLKYGKCYFWSNEMKGSWSDSYVYCLERKSHLL 100

Qy 112 TFPNQGVNLFQEVGE--DFYWIGLRID--GWRWEDGPAISLSIL-----SNSVYVQ 160
Db 101 IHHQLEMAFIQKRLQNLQVYVYIGLNTSLKMTWTWVDGSPIDSKIPKIPKPAKENS--- 157

Qy 161 KGTIHRGCLHASCEVALQWICE 184
Db 158 -CAAKESKIFSETCSSVFKWICQ 180

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RESULT 4
O54708

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ID O54708 PRELIMINARY; PRT; 179 AA.
AC O54708;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE CD94.
GN KLRD1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; PubMed=9464811;
RX MEDLINE=98124458;
RA Vance R.E., Tanamachi D.M., Hanke T., Raullet D.H.;
RT "Cloning of a mouse homolog of CD94 extends the family of C-type
RT lectins on murine natural killer cells.";
RL Eur. J. Immunol. 27:3236-3241(1997).
DR EMBL; AF030312; AAC28244.1; -.
DR MGD; MGI:1196275; Klrcl.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SQ SEQUENCE 179 AA; 20809 MW; D59E1CB63139E45 CRC64;

Query Match 16.9%; Score 175; DB 11; Length 179;
Best Local Similarity 27.9%; Pred. No. 1.3e-10;
Matches 50; Conservative 36; Mismatches 71; Indels 22; Gaps 10;

QY 22 SRWKYKAVLHR-PCVSYLVVMVALGLLTIVILMSLLYQRTLC-CGSKGFM-CSQCSKCPNL 78
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
7 TRWRLMSVIFGIKCL--FLMVTGLVLLINSFTIQISTPSTPTTTFVFEQVSECCVCLDK 64

QY 79 WWRNGSHCYFYSKEKRDWNSLKFCADKGSLLITFPDNOGVNLFQYVGBDFWIGL--- 135
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
65 WVGHCNCYFISKEEKSRSRDFCASQNSLLQ-PQSRNELSFMNF-SQTFWIGMHYS 122

QY 136 RIDDGNRWDGDPALSLISLN-SVQKCGTHRC-----GLHASSCEVALQWICEKV 186
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
123 EKRNALWEDGTVPKDLFPFVSIRP-----EHCIVSPSKSVSAESCENKRYICKKL 177

RESULT 5
O54707 PRELIMINARY; PRT; 179 AA.
AC O54707;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Killer cell lectin-like receptor, subfamily D, member 1 (CD94).
GN KLRD1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Vance R.E., Tanamachi D.M., Hanke T., Raullet D.H.;
RL Eur. J. Immunol. 27:0-0(1997).
DR [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Heusel J.W., Ho E.L., Brown M.G., Matsumoto K., Yokoyama W.M.;
RT "Murine CD94.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).
DR [3]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Butcher S., Cottage A., Cook G.P.;
RT "Mouse natural killer cell receptors homologous to human CD94 and
RT NKG2-D.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030311; AAC28243.1; -.
DR EMBL; AF057714; AAC33713.1; -.
DR EMBL; AF039025; AAD02116.1; -.
DR MGD; MGI:1196275; Klrcl.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Lectin.
SQ SEQUENCE 179 AA; 20808 MW; DD343419E93B3465 CRC64;

Query Match 16.9%; Score 175; DB 11; Length 179;
Best Local Similarity 27.9%; Pred. No. 1.3e-10;
Matches 50; Conservative 36; Mismatches 71; Indels 22; Gaps 10;

QY 22 SRWKYKAVLHR-PCVSYLVVMVALGLLTIVILMSLLYQRTLC-CGSKGFM-CSQCSKCPNL 78
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
7 TRWRLMSVIFGIKCL--FLMVTGLVLLINSFTIQISTPSTPTTTFVFEQVSECCVCLDK 64

QY 79 WWRNGSHCYFYSKEKRDWNSLKFCADKGSLLITFPDNOGVNLFQYVGBDFWIGL--- 135
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
65 WVGHCNCYFISKEEKSRSRDFCASQNSLLQ-PQSRNELSFMNF-SQTFWIGMHYS 122

QY 136 RIDDGNRWDGDPALSLISLN-SVQKCGTHRC-----GLHASSCEVALQWICEKV 186
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
123 EKRNALWEDGTVPKDLFPFVSIRP-----EHCIVSPSKSVSAESCENKRYICKKL 177

RESULT 6
Q9R007 PRELIMINARY; PRT; 165 AA.
AC Q9R007;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Type II transmembrane protein MDL-1 (C-type).
GN CLECSF5 OR MDL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Myeloid;
RX MEDLINE=99380598; PubMed=10449773;
RA Bakker A.B., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.;
RT "Myeloid DAP12-associated lectin (MDL)-1 is a cell surface receptor
RT involved in the activation of myeloid cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9792-9796(1999).
DR [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF139769; AAF02492.1; -.
DR EMBL; AK036697; BAC29537.1; -.
DR MGD; MGI:1345151; Clec5f5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.

```

DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Transmembrane.
SQ SEQUENCE 165 AA; 19055 MW; 626D64392A513282 CRC64;

Query Match
Best Local Similarity 16.7%; Score 173; DB 11; Length 165;
Matches 47; Conservative 28; Mismatches 61; Indels 30; Gaps 6;

Qy 40 MVALGLTLVIMSL-----LLY-----QRLCCGSKGFMCSQCSRCNLMWRNGSH 85
Db 5 MIISGLIVVIVKVGMTFFLLYFSQIFGRNDESTMPTRSYGT-----CPRNWDFHQGK 58
Qy 86 CYFESMEKRDWNSLSKFCADKSHLLTFPPDNQGNLFQEVYGEDFYWIGLRDIDG---WR 142
Db 59 CFFFSFSESPWKSDMDYCATQGSTLAIVNTPEKLYLQDIAGIENYFGLVRQPGCKWR 118
Qy 143 WEDGALSLSLTSLNSVVKCGTIHRCGL-----HASSCEVALQWICE 184
Db 119 WINNSVFNQVNTQDNQDFCVTI---GLTKTYDAASCEVSYRWICE 161

RESULT 7
Q9GLF4 PRELIMINARY; PRT; 165 AA.
AC Q9GLF4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Myeloid DAP12-associating lectin short form.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21308528; PubMed=11414735;
RA Yim D., Jie H.B., Sotiriadis J., Kim Y.S., Kim Y.B.;
RT "Molecular cloning and expression pattern of porcine myeloid DAP12-
associating lectin-1".
RT Cell. Immunol. 209:42-48(2001).
DR EMBL; AF285449; AAG29427.1; -;
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 165 AA; 18653 MW; 40C29ABE136E76D3 CRC64;

Query Match
Best Local Similarity 16.5%; Score 171; DB 6; Length 165;
Matches 47; Conservative 27; Mismatches 69; Indels 18; Gaps 5;

Qy 40 MVALGLTLVIL-----MSLLYQRLTCCGSKGFMCSQCSRCNLMWRNGSHCYFSPM 91
Db 5 MIISGLIVVIVKVGMTFFLLYFSQIFGSSNVSTFTPTSGVTCPTGWDHFQGRCFLLST 64
Qy 92 EKRDWNSLSKFCADKSHLLTFPPDNQGNLFQEVYGEDFYWIGLRDIDG---WRWEDGPA 148
Db 65 SENSWNNSMNFCKQGSTLAIVNTPEKLYLQDIAGIENYFGLVRQPGCKWRWINNS 124
Qy 149 LSLTSLNSVVKCGTIHRCGL-----HASSCEVALQWICEK 185
Db 125 FNGSVISHSHFNVCVTI---GLTKTFDAASCDVNSRICEK 162

RESULT 8
Q8BL24 PRELIMINARY; PRT; 164 AA.
ID Q8BL24
AC Q8BL24;

DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE C-type.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose tissue;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs".
RT Nature 420:563-573(2002).
RL EMBL; AK046600; BAC32802.1; -;
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 164 AA; 18927 MW; DF0AE012C049C1C0 CRC64;

Query Match
Best Local Similarity 16.0%; Score 165.5; DB 11; Length 164;
Matches 48; Conservative 28; Mismatches 59; Indels 31; Gaps 7;

Qy 40 MVALGLTLVIMSL-----LLY-----QRLCCGSKGFMCSQCSRCNLMWRNGSH 85
Db 5 MIISGLIVVIVKVGMTFFLLYFSQIFGRNDESTMPTRSYGT-----CPRNWDFHQGK 58
Qy 86 CYFESMEKRDWNSLSKFCADKSHLLTFPPDNQGNLFQEVYGEDFYWIGLRDIDG---WR 142
Db 59 CFFFSFSESPWKSDMDYCATQGSTLAIVNTPEKLYLQDIAGIENYFGLVRQPGCKWR 117
Qy 143 WEDGALSLTSLNSVVKCGTIHRCGL-----HASSCEVALQWICE 184
Db 118 WINNSVFNQVNTQDNQDFCVTI---GLTKTYDAASCEVSYRWICE 160

RESULT 9
Q95JG4 PRELIMINARY; PRT; 161 AA.
ID Q95JG4;
AC Q95JG4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Natural killer cell receptor protein 1 variant 1 (Fragment).
GN KLRB1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=21351526; PubMed=11457486;
RA Govaerts M.M., Goddeeris B.M.;
RT "Homologues of natural killer cell receptors NKG2-D and NKR-P1
expressed in cattle".
RL Vet. Immunol. Immunopathol. 80:339-344(2001).
DR EMBL; AF322886; AAK73811.1; -;
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
FT NON_TER 1 1


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FT NON TER 161 161
SQ SEQUENCE 161 AA; 18648 MW; 24F9AA4A19EAFB7 CRC64;

Query Match
Best Local Similarity 15.9%; Score 165; DB 6; Length 161;
Matches 38; Conservative 19; Mismatches 56; Indels 8; Gaps 4;

QY 75 CPNLMWRNGSHCYFSEMEKEDWNSLKFCDKDGSHLLTFPDNQGNLFOEYVGED--FYW 132
Db 41 CPWHKRIKDCYFSTSPKNDLADCTRESSLLIQDQELRLQMQLNKGLFW 100
QY 133 IGLR-DIDG---WRWEDGPALS---LSILSNSVVGKGTTHRCGLHASSCEVALQWICEKV 186
Db 101 IGLNFTLSGSKRWINGSFLNSLILPFGDAKEDCCVYISKTCISDYCAAKRWICQKE 160
QY 187 L 187
Db 161 L 161

RESULT 10
Q9GLF3 PRELIMINARY; PRT; 185 AA.
AC Q9GLF3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myeloid DAPI2-associating lectin long form.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21308528; PubMed=11414735;
RA Yim D., Jie H.B., Sotiriadis J., Kim Y.S., Kim Y.B.;
RT "Molecular cloning and expression pattern of porcine myeloid DAPI2-
RT associating lectin-1";
RL Cell. Immunol. 209:42-48(2001).
DR EMBL; AF285450; AAG29428.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 185 AA; 20835 MW; DA6EC0AF58BC95CE CRC64;

Query Match
Best Local Similarity 15.8%; Score 164; DB 6; Length 185;
Matches 49; Conservative 22; Mismatches 72; Indels 38; Gaps 5;

QY 40 MVALGLLTVLIL---MSLLIYQRTLCCKSGKGFMCSCQR----- 74
Db 5 MIISGLIVVVLKLVGVTFFLLYPQIFGEHNVFSFSTPRTGTVQIFGSGNSFTTESF 64
QY 75 ---CPNLMWRNGSHCYFSEMEKEDWNSLKFCDKDGSHLLTFPDNQGNLFOEYVGEDFY 131
Db 65 GTVCPGTGWDPHQRCFPFLSTSENSWNNMNFCKQKGTSLAIVNTPKLFQINISGAEKY 124
QY 132 WIGURDIDG---WRWEDGPALSLSILSNSVVGKGTTHRCGL-----HASSCEVALQWICE 184
Db 125 FGLLYQPAEKMRWINNSVFNFSVISHNFNCVTI---GLTKTFDAASCVDNYRSICE 181
QY 185 K 185
Db 182 K 182

RESULT 11
Q8MHY8 PRELIMINARY; PRT; 179 AA.
ID Q8MHY8
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Q8MHY8;
AC Q8MHY8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Natural killer cell receptor.
GN POPY-CD94.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470381; AAM78481.1; -.
DR EMBL; AF470382; AAM78482.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20550 MW; 6752CB8F182CFD73 CRC64;

Query Match
Best Local Similarity 15.6%; Score 161.5; DB 6; Length 179;
Matches 48; Conservative 25; Mismatches 84; Indels 19; Gaps 7;

QY 24 WKYKAVLHPRCVSYLWVALGILLTVILSLIYQRTLCCKG-----SKGFMCSCQSCPNI 78
Db 10 WLISGTLGIICLS--LMATLIGILLKNSFTKLSTIEPAFTPGDIELOKD---SPCCSCQEK 64
QY 79 WMRNGSHCYFSEMEKEDWNSLKFCDKDGSHLLTFPDNQGNLFOEYVGEDFYWIGL--- 135
Db 65 WVGRCNCYFISSEQKTWNEHRLCASQKSSLLQLQNTDELDPMS--SQQFWIGLSYS 122
QY 136 RIDGWRWEDGPALS---LSILSNSVVGKGTTHRCG-LHASSCEVALQWICEKV 187
Db 123 EETAWLWENGSAISQYLFELFETFPKNCIAYPNPENGALDESCDKRYICKQOL 178

RESULT 12
Q8WUP7 PRELIMINARY; PRT; 154 AA.
ID Q8WUP7
AC Q8WUP7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to lectin-like NK cell receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Testis;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019883; AAH19883.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
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```
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20566 MW; 6752CB8F0F9A2609 CRC64;

Query Match 15.3%; Score 158.5; DB 6; Length 179;
Best Local Similarity 26.7%; Pred. No. 7.5e-09;
Matches 47; Conservative 26; Mismatches 84; Indels 19; Gaps 7;

Qy 24 WKVKAVLHRPCVSYLVVVALGLLTVILMSLLLYQRTILCCG-----SKGFMCSCQSCRCPNL 78
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 10 WLISGTLGIICLS--LMATLGIILKNSFTKLSIEPAFTPGPDIELQKD---SDCCSCQEK 64

Qy 79 WMRNGSHCYFESMEKRDWNSSLKECADKSGHLLTFPDNQGVNLFQEVYVGEDFYWIGL--- 135
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 65 WVGRCNCYFISSEQKTWNESRHLCASQKSLLOLQNTDELDFMSS--SQQFYWIGLSYS 122

Qy 136 RDIDGWZWDGPALS---LSILSNSVVKCGTIHRCG-LHASSCEVALQWICEKVL 187
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 123 EEHTAWLWENGSSLSQYLFLPFTFPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
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Search completed: August 10, 2004, 16:44:03
Job time : 32 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:35:35 ; Search time 47.5 Seconds
(without alignments)
1118.293 Million cell updates/sec

Title: US-09-811-367B-5

Perfect score: 1036

Sequence: 1 MADNSYSTLELPAARVQD.....GLHASCEVALQWICKVLP 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1082526

Minimum DB seq length: 0
Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1980s:*
- 3: geneseqp2000s:*
- 4: geneseqp2000s:*
- 5: geneseqp2000s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2	AAR77033 Mammalian
2	1036	100.0	188	2	AAW89277 Rat mast
3	1036	100.0	188	4	AAE11761 Rat mast
4	838	80.9	188	4	AAE11760 Mouse mas
5	651	62.8	114	2	AAE117472 Partial s
6	207.5	20.0	99	2	AAW88267 Human MAF
7	170	16.4	165	4	AAU00673 Human INT
8	170	16.4	165	6	ABO32541 Secreted
9	164.5	15.9	182	4	AAU19660 Human nov
10	164.5	15.9	182	5	ABP47880 Human pol
11	164.5	15.9	182	7	ADC10842 Human ext
12	163.5	15.8	142	4	AAW80296 Human pro
13	163.5	15.8	142	6	ABG72616 Human Cyt
14	163.5	15.8	160	4	AAW80302 Human pro
15	163	15.7	160	4	AAU00675 Human INT
16	163	15.7	145	6	ABO32547 Secreted
17	161	15.5	181	2	AAW27288 Human G52
18	161	15.5	181	7	ADC38664 Human sec
19	160	15.4	162	2	AAV27446 Human SDC
20	159.5	15.4	188	4	AAW78675 Human pro
21	159.5	15.4	188	4	AAU00671 Human INT
22	159.5	15.4	188	6	ABO32533 Secreted
23	158.5	15.3	167	2	AAW63022 Mouse dec
24	156.5	15.1	149	2	AAW36957 Protein e
25	155	15.0	179	2	AAW64791 Human Kp4

26	155	15.0	179	2	AAW40222	AAW40222	CD34.	7/1
27	155	15.0	179	8	ADE76965	ADE76965	Human pro	
28	154	14.9	138	6	ABO32543	ABO32543	Secreted	
29	154	14.9	162	6	ABO32535	ABO32535	Secreted	
30	153.5	14.8	140	4	AAU19836	AAU19836	Human nov	
31	153.5	14.8	140	4	AAU19690	AAU19690	Human nov	
32	153.5	14.8	140	4	ABBI5422	ABBI5422	Human ner	
33	153.5	14.8	140	4	ABBI7909	ABBI7909	Human ner	
34	153.5	14.8	140	5	ABP48056	ABP48056	Human pol	
35	153.5	14.8	140	5	ABP47910	ABP47910	Human pol	
36	153.5	14.8	140	7	ADC10872	ADC10872	Human ext	
37	153.5	14.8	140	7	ADC11018	ADC11018	Human pro	
38	153.5	14.8	149	2	AAW64544	AAW64544	Human lym	
39	153.5	14.8	149	2	AAW75877	AAW75877	Type II m	
40	153.5	14.8	149	2	AAW85592	AAW85592	Human C-t	
41	153.5	14.8	149	5	ABB09713	ABB09713	Amino aci	
42	153.5	14.8	149	7	ADC38674	ADC38674	Human sec	
43	153	14.8	126	2	AAW63013	AAW63013	Mouse dec	
44	153	14.8	133	5	AAU72822	AAU72822	Human NKG	
45	153	14.8	143	5	AAU72821	AAU72821	Human NKG	

ALIGNMENTS

RESULT 1

AAAR77033
ID AAR77033 standard; protein; 188 AA.

XX AAR77033;

DT 01-FEB-1996 (first entry)

DE Mammalian mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA; soluble; ligand;

KW identification; screening; inflammation; inflammatory; allergy; allergic;

KW prevention.

XX Rattus rattus.

XX WO9527734-A1.

XX 19-OCT-1995.

XX 06-APR-1995; 95WO-US004258.

XX 08-APR-1994; 94IL-00109257.

XX (YEDA) YEDA RES & DEV CO LTD.

XX (RYCU/) RYCUS A.

XX Pecht I, Guthmann MD, Tal M;

XX WPI; 1995-366356/47.

XX N-PSDB; AAT01471.

XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
of inflammatory and allergic reactions.

XX Claim 12; Page 37; 54pp; English.

XX A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions

XX Sequence 188 AA;

Query Match

Best Local Similarity 100.0%; Score 1036; DB 2; Length 188;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSYLVVMVALGLLTIVILMSLLLYQRTL 60
Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSYLVVMVALGLLTIVILMSLLLYQRTL 60
QY 61 CCGSGKPMCSQCRCPNLWMRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFFDNQGVN 120
Db 61 CCGSGKPMCSQCRCPNLWMRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFFDNQGVN 120
QY 121 LFQYVGEDFYWIGLRDIDGWRWEDGPAISLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
Db 121 LFQYVGEDFYWIGLRDIDGWRWEDGPAISLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVLP 188
Db 181 WICEKVLP 188
RESULT 2
AAW88277
ID AAW88277 standard; protein; 188 AA.
AC AAW88277;
XX 29-MAR-1999 (first entry)
DT 29-MAR-1999 (first entry)
DE Rat mast cell function-associated antigen (MAFA).
XX Mast cell function-associated antigen; MAFA; splice variant; rat;
KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX Rattus sp.
FH Key Location/Qualifiers
FT Modified-site 82..84
FT /note= "Asn is N-glycosylated"
FT Modified-site 97..99
FT /note= "Asn is N-glycosylated"
XX WO9854209-A2.
XX 03-DEC-1998.
XX 29-MAY-1998; 98WO-GB001572.
XX 31-MAY-1997; 97GB-00011148.
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX WPI; 1999-059806/05.
XX N-PSDB; AAW84222.
XX New polypeptide having a sequence corresponding to human mast cell
PT function-associated antigen - useful in forming and manufacturing
PT pharmaceutical compositions in the treatment of inflammatory and allergic
PT diseases, and tumour growth.
XX Disclosure; Fig 4; 44pp; English.
XX This is the amino acid sequence of rat mast cell function-associated
CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and
CC basophils. The invention relates to cloning of the human MAFA molecule
CC (see AAW88265) and to the discovery of splice variants (see AAW88266-67)
CC of human MAFA that are not found in rat. Polypeptides and synthetic
CC peptides (see AAW88258-64) based on human MAFA and human truncated MAFA,
CC and polynucleotides encoding them, can be used in methods for the
CC treatment of inflammatory and allergic diseases (e.g. rheumatoid
CC arthritis and asthma), and tumour growth
XX Sequence 188 AA;
SQ

Query Match 100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.8e-96;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSYLVVMVALGLLTIVILMSLLLYQRTL 60
Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRCPCVSYLVVMVALGLLTIVILMSLLLYQRTL 60
QY 61 CCGSGKPMCSQCRCPNLWMRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFFDNQGVN 120
Db 61 CCGSGKPMCSQCRCPNLWMRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFFDNQGVN 120
QY 121 LFQYVGEDFYWIGLRDIDGWRWEDGPAISLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
Db 121 LFQYVGEDFYWIGLRDIDGWRWEDGPAISLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVLP 188
Db 181 WICEKVLP 188
RESULT 3
AAE11761
ID AAE11761 standard; protein; 188 AA.
AC AAE11761;
XX 18-DEC-2001 (first entry)
DT 18-DEC-2001 (first entry)
DE Rat mast cell function-associated antigen (MAFA) protein.
XX Rat; pharmaceutical composition; mast cell function associated antigen;
KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KW immunosuppressive; cytostatic.
XX Rattus norvegicus.
OS WO200170805-A2.
XX 27-SEP-2001.
XX 16-MAR-2001; 2001WO-US008596.
XX 17-MAR-2000; 2000US-0190716P.
XX (GEMI-) GEMINI SCI INC.
XX Takahashi N, Mikayama T;
XX WPI; 2001-611482/70.
XX N-PSDB; AAD18736.
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
PT activity of natural killer cell or T-cell, comprises an agent that binds
PT to mast cell function-associated antigen ligand on target cell.
XX Example 1; Page 19; 49pp; English.
XX The present invention relates to a pharmaceutical composition comprising
CC an agent which specifically binds to a mast cell function associated
CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
CC ligand and a pharmaceutically acceptable excipient. The invention is
CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
CC binding to a ligand on a target cell, by contacting the pharmaceutical
CC composition in vitro, ex vivo or in vivo by administering the composition
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
CC on the target cell. The agent or the composition is useful for treating a
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of
CC NK cell or a T-cell. The present sequence is rat MAFA protein

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XX SQ Sequence 188 AA;
Query Match 100.0%; Score 1036; DB 4; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.8e-96;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLRPCVSVLVMVALGLLTIVILMSLLLYQRTL 60
DB 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLRPCVSVLVMVALGLLTIVILMSLLLYQRTL 60

QY 61 CCGSGKGFMCQCSRCPNLWNRNGSHCYFYSMEKRDWNSLSLKFCADKGSLLTTPDNOGVN 120
DB 61 CCGSGKGFMCQCSRCPNLWNRNGSHCYFYSMEKRDWNSLSLKFCADKGSLLTTPDNOGVN 120

QY 121 LFOBYVGEDFYWIGLRIDGWRWEDGPALSLILNSVVOCKGTHRCGLHASSCEVALQ 180
DB 121 LFOBYVGEDFYWIGLRIDGWRWEDGPALSLILNSVVOCKGTHRCGLHASSCEVALQ 180

QY 181 WICEKVLP 188
DB 181 WICEKVLP 188

RESULT 4
ID AAE11760 standard; protein; 188 AA.
XX AAE11760;
XX AAE11760;
DT 18-DEC-2001 (first entry)
DE Mouse mast cell function associated antigen (MAFA) protein.
XX Mouse; pharmaceutical composition; mast cell function associated antigen;
XX MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
XX immunosuppressive; cytostatic.
XX Mus sp.
XX Key Location/Qualifiers
FH Domain 64..188
FT /note="Extracellular domain"
XX
XX WO200170805-A2.
XX
XX 27-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US008596.
XX
XX 17-MAR-2000; 2000US-0190716P.
XX
XX (GEMI-) GEMINI SCI INC.
XX
XX Takahashi N, Mikayama T;
XX
XX WPI; 2001-611482/70.
XX
XX N-PSDB; AAD18735.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
XX activity of natural killer cell or T-cell, comprises an agent that binds
XX to mast cell function-associated antigen ligand on target cell.
XX
XX Example 1; Page 19; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
XX an agent which specifically binds to a mast cell function associated
XX antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
XX killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
XX ligand and a pharmaceutically acceptable excipient. The invention is
XX useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
XX binding to a ligand on a target cell, by contacting the pharmaceutical
XX composition in vitro, ex vivo or in vivo by administering the composition
XX
XX CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
XX an amount sufficient to inhibit cell surface MAFA binding to the ligand
XX on the target cell. The agent or the composition is useful for treating a
XX tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
XX T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
XX tumour cell. The invention is also useful for inhibiting an activity of
XX NK cell or a T-cell. The present sequence is mouse MAFA protein
XX SQ Sequence 188 AA;
Query Match 80.9%; Score 838; DB 4; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.9e-76;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLRPCVSVLVMVALGLLTIVILMSLLLYQRTL 60
DB 1 MADSSIYSTLELPEAQVQDQSRWKLKAVLRHPLSRFAMVALGLLTIVILMSLLMYQRL 60

QY 61 CCGSGKGFMCQCSRCPNLWNRNGSHCYFYSMEKRDWNSLSLKFCADKGSLLTTPDNOGVN 120
DB 61 CCGSKDSTCSHCPCPILWTRNGSHCYFYSMEKRDWNSLSLKFCADKGSLLTTPDNOGVK 120

QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLILNSVVOCKGTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGEDFYWIGLRIDGWRWEGGPALSLRLTNSLQRCGAIHRNGLQASCEVALQ 180

QY 181 WICEKVLP 187
DB 181 WICKKVL 187

RESULT 5
ID AAR77472 standard; protein; 114 AA.
XX AAR77472
XX AAR77472;
XX AAR77472;
DT 01-FEB-1996 (first entry)
DE Partial sequence of mast cell function-associated antigen (MAFA) .
XX Mast cell function-associated antigen; MAFA; soluble; ligand;
XX identification; screening; inflammation; inflammatory; allergy; allergic;
XX prevention.
XX Rattus rattus.
XX OS
XX WO9527734-A1.
XX PN
XX 19-OCT-1995.
XX PD
XX 06-APR-1995; 95WO-US004258.
XX PF
XX 08-APR-1994; 94IL-00109257.
XX PR
XX (YEDA ) YEDA RES & DEV CO LTD.
XX PA (RYCU/) RYCUS A.
XX PI
XX Pecht I, Guthmann MD, Tal M;
XX WPI; 1995-366356/47.
XX DR N-PSDB; AAT01471.
XX
XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
XX useful for screening for ligands of MAFA which are useful for prevention
XX of inflammatory and allergic reactions.
XX Disclosure; Page 38; 54pp; English.
XX
XX A soluble form of mast cell function-associated antigen (MAFA) can be
XX produced by recombinant techniques for use in the ligand- screening
XX assay. The ligands that are identified may be used alone or in
XX combination with the MAFA to prevent inflammatory and allergic reactions

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XX SQ Sequence 114 AA;
Query Match 62.8%; Score 651; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.1e-58;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 CPNLMWRNGSHCYFFSMKRDWNSLKFCADKSGHLLTFPDNQGVLFOEYVGEDFYWIG 134
DB 1 CPNLMWRNGSHCYFFSMKRDWNSLKFCADKSGHLLTFPDNQGVLFOEYVGEDFYWIG 60

QY 135 LRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQWICEKVL 188
DB 61 LRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQWICEKVL 114

RESULT 6
AAW88267
ID AAW88267 standard; protein; 99 AA.
XX AC AAW88267;
XX DT 29-MAR-1999 (first entry)
XX DE Human MAFA splice variant huMAFA(E3/4-).
XX KW Mast cell function-associated antigen; MAFA; huMAFA(E3/4-);
XX KW splice variant; human; inflammation; allergy; asthma;
XX KW rheumatoid arthritis; tumour; therapy.
XX OS Homo sapiens.
XX PN WO9854209-A2.
XX PD 03-DEC-1998.
XX PF 29-MAY-1998; 98WO-GB001572.
XX PR 31-MAY-1997; 97GB-00011148.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX DR WPI; 1999-059806/05.
XX DR N-PSDB; AAW84200.
XX PT New polypeptide having a sequence corresponding to human mast cell
XX PT function-associated antigen - useful in forming and manufacturing
XX PT pharmaceutical compositions in the treatment of inflammatory and allergic
XX PT diseases, and tumour growth.
XX PS Disclosure; Fig 3; 44pp; English.
XX CC This is the amino acid sequence of human mast cell function- associated
XX CC antigen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-
XX CC like domain of human MAFA (see AAW88265) but retains the intracellular
XX CC and transmembrane domains as well as the extracellular C-terminal tail.
XX CC Truncated MAFA polypeptides including huMAFA(E3/4-), and polynucleotides
XX CC encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-
XX CC 72), can be used in compositions for the treatment of
XX CC inflammatory and allergic diseases (e.g. rheumatoid arthritis and
XX CC asthma), or tumour growth
XX SQ Sequence 99 AA;
Query Match 20.0%; Score 207.5; DB 2; Length 99;
Best Local Similarity 29.6%; Pred. No. 4.7e-13;
Matches 55; Conservative 12; Mismatches 30; Indels 89; Gaps 1;

QY 1 MADNSTYSTLELPAAPRVODDSRWKVKAVLHRCVSLVWVAIGLLTIVLMSLLLYQRTL 60
DB 1 MTDSTIYSMLLELPTATQANDYGPQKSSSRPSCSLVAIGLLTAVLLSVLLYQWL 60

QY 61 CCGSKGFMCSCSRCPNLWMRNGSHCYFFSMKRDWNSLKFCADKSGHLLTFPDNQGVL 120
DB 61 CCG----- 63
QY 121 LFQBYVGEDFYWIGLRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQ 180
DB 64 -----ISSNSFVQTGATTKNGLOASSCEVPLH 91
QY 181 WICEKV 186
DB 92 WVCKKV 97

RESULT 7
AAU00673
ID AAU00673 standard; protein; 165 AA.
XX AC AAU00673;
XX DT 07-SEP-2001 (first entry)
XX DE Human INTERCEPT 289 form 2a polypeptide.
XX KW Human; INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain;
XX KW skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;
XX KW bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;
XX KW anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease;
XX KW malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
XX KW attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
XX KW hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
XX KW muscular dystrophy; immuno-competence; vertebrae; blood; serum; lung.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 7..27
XX FT /note= "Transmembrane domain"
XX FT Domain 28..165
XX FT /note= "Extracellular domain"
XX PN WO200129088-A1.
XX PD 26-APR-2001.
XX PF 23-JUN-2000; 2000WO-US017386.
XX PR 19-OCT-1999; 99US-00420707.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Mackay CR, Myers PS, Kirst SJ, Fraser CC, Leiby KH;
XX DR WPI; 2001-308477/32.
XX DR N-PSDB; AAS00663.
XX PT New isolated nucleic acid molecule for diagnosis, prevention, and therapy
XX PT of human and other animal disorder, or as modulating agent for regulating
XX PT cellular processes.
XX PS Claim 8; Fig 2H-2I; 263pp; English.
XX CC The sequence represents human INTERCEPT 289 form 2a polypeptide. This
XX CC protein and similar others exhibit the ability to affect growth,
XX CC proliferation, survival, differentiation, activity, morphology, or
XX CC movement/migration of, e.g. T cells and cells of the heart, liver,
XX CC pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph
XX CC node, peripheral blood leukocyte, bone marrow or thymus tissues. They can
XX CC be used as modulating agents for regulating cellular processes, thus, the
XX CC proteins and their associated nucleic acids can be used to prognosticate,
XX CC prevent, diagnose, or treat disorders associated with physiological
XX CC processes. These disorders include abnormal blood coagulation, asthma,
XX CC anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery
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PR 20-OCT-2000; 2000US-02411786P.
PR 20-OCT-2000; 2000US-02411787P.
PR 20-OCT-2000; 2000US-02411808P.
PR 20-OCT-2000; 2000US-02411809P.
PR 20-OCT-2000; 2000US-02411826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764870.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2003-743765/70.
XX N-PSDB; ADC10577.
XX
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
XX treating, and/or preventing disorders, such as cancer, infections,
XX cardiovascular and inflammatory diseases.
XX
XX Claim 11; SEQ ID NO 310; 235pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (cDNA)
XX encoding a human extracellular matrix protein, representing one of 161
XX novel genes. Also included are recombinant vectors, host cells
XX (expressing the protein), the extracellular matrix proteins (including
XX
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CC their fragments, epitopes and homologues), an isolated antibody that
CC binds specifically to the protein, diagnosing a pathological condition or
CC susceptibility to a pathological condition (comprising determining the
CC presence or absence of a mutation in the nucleic acid and diagnosing a
CC condition based on the presence or absence of the mutation), diagnosing a
CC pathological condition or susceptibility to a pathological condition
CC (comprising determining the presence or amount of expression of the
CC protein in a biological sample and diagnosing a condition based on the
CC presence or amount of expression of the protein), preventing, treating or
CC ameliorating a medical condition by administering the nucleic acid or
CC protein to a mammalian subject, identifying a binding partner to the
CC protein, the gene corresponding to the cDNA sequence, and identifying an
CC activity in a biological assay (comprising expressing the nucleic acid in
CC a cell, isolating the supernatant, detecting an activity in a biological
CC assay and identifying the protein in the supernatant having the
CC activity). The nucleic acids and proteins display the following
CC activities: Cytostatic, antibacterial, Virucide, Neuroprotective,
CC Gynaecological, Gastrointestinal-Gen, Cardiant, Cardiovascular-Gen,
CC Nephrotropic, Antiinflammatory, Muscular-Gen, Respiratory-Gen,
CC
Query Match 15.9%; Score 164.5; DB 7; Length 182;
Best Local Similarity 26.9%; Pred. No. 2.2e-08;
Matches 36; Conservative 22; Mismatches 59; Indels 17; Gaps 5;
QY 62 CGSKGFMCSOCRCPLNWMENGSHCYFYSMEKRDWNSLKFCADKGSHLLTFPDNQGVNL 121
Db 54 CASRS--ADQTVLCQSEWLKYGKCYWFSNEMKSWSDSYVYCLERKSHLLIHDLEMAF 111
QY 122 FOEYVGE-DFYVIGLRDID---QWRWEDGFPALSLIL-----SNSVWQKCGTHRCGL 170
Db 112 IQNLRQLNYYVIGLNFNTSLKMTWTWVDGSPIDSKIFFIKGPAKENS---CAAIKESKI 167
QY 171 HASCEVALOWICE 184
Db 168 FSETCSSVFEWICQ 181
RESULT 12
AA80296
ID AA80296 standard; protein; 142 AA.
XX
XX AA80296;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human protein SEQ ID NO 3948.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX 20-JUN-2000; 2000US-00598075.
XX 19-JUL-2000; 2000US-00620325.
XX 01-SEP-2000; 2000US-00654936.
XX 15-SEP-2000; 2000US-00663561.
XX 20-OCT-2000; 2000US-00693325.
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
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PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAK53429.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 PS Claim 20; Page 6210-6211; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 142 AA;

Query Match 15.8%; Score 163.5; DB 4; Length 142;
 Best Local Similarity 26.1%; Pred. No. 2.1e-08;
 Matches 40; Conservative 25; Mismatches 67; Indels 21; Gaps 5;
 QY 38 LVMVALGLTLVILMSLLLYQRTLCGSGKGFMCSCRCFNLWMRNGSHCYFYSMEKRDWN 97
 DB 3 VLLAVSGVIVVLASR-----AGAR-----CQCPGPGWVLSSEHCYFYSAAQAW 48
 QY 98 SSLKFCADKSGHLLTFPDNQGNVLFQFYVGDYFVIGL-RDIDGWRWEDGPALSIL-- 154
 DB 49 ASQAFCSAYHATLPLLSHTQ--DFLGRYPVSRHSWVGAWRPGQWHWIDEAPLPQLLPE 106
 QY 155 --SNSVQKCGTIHRCGHHASCEVALQWICEK 185
 DB 107 DGEDNLDINCALBEGTLVAANCSTPRPFWCAK 139

RESULT 13
 ABG72616
 ID ABG72616 standard; protein; 142 AA.
 XX
 AC ABG72616;
 XX
 DT 12-FEB-2003 (first entry)
 XX
 XX Human cytokine or cell proliferation/differentiation protein #6.
 DE
 DE Human; cytokine; cell proliferation; cell differentiation; anaemia;
 KW wound; ulcer; thrombocytopaenia; osteoporosis; osteoarthritis;
 KW inflammation; Alzheimer's disease; Parkinson's disease; stroke;
 KW Huntington's disease; amyotrophic lateral sclerosis; HIV;
 KW immune deficiency; human immunodeficiency virus infection;
 KW severe combined immunodeficiency; infection; autoimmune disorder;
 KW rheumatoid arthritis; Guillain-Barre syndrome; graft-versus-host disease;
 KW cancer; thyroid cancer; lung cancer; small cell carcinoma;
 KW Kaposi's sarcoma; brain tumour; prostate cancer; ovarian cancer;
 KW leukaemia; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; food supplement.
 KW
 XX Homo sapiens.
 OS

US2002137044-A1.

26-SEP-2002.

30-JAN-2001; 2001US-00774434.

PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (TANG/) TANG Y T.
 PA (ZHOU/) ZHOU P.
 PA (GOOD/) GOODRICH R.
 PA (LIUC/) LIU C.
 PA (ASUN/) ASUNDI V.
 PA (WEHR/) WEHRMAN T.
 PA (YANG/) YANG Y.
 PA (DRMA/) DRMANAC R T.
 XX
 PI Tang YT, Zhou P, Goodrich R, Liu C, Asundi V, Wehrman T, Yang Y;
 PI Drmanac RT;
 DR WPI; 2003-110596/10.
 DR N-PSDB; ABX13629.
 XX
 CC New polynucleotides for diagnosing, treating or preventing e.g. anemia,
 CC wounds, ulcers, thrombocytopenia, osteoporosis, inflammations,
 CC Alzheimer's disease, stroke, autoimmune disorders or cancers.
 PT
 PT
 PS Claim 19; Page 60; 63pp; English.
 XX

CC The invention relates to an isolated polynucleotide encoding a cytokine
 CC or cell proliferation/differentiation-related protein (or the mature
 CC protein or active domain), sequences greater than 90% identical to it or
 CC sequences complementary to it. Also included are the encoded proteins,
 CC expression vectors, transformed host cells, antibodies, and identifying a
 CC compound that binds to the polypeptide. The polynucleotide, polypeptides
 CC encoded by it, or antibodies to the polypeptides are useful in
 CC therapeutic, diagnostic or research methods. They are particularly useful
 CC for diagnosing, treating or preventing e.g. anaemias, wounds, ulcers,
 CC thrombocytopaenia, osteoporosis, osteoarthritis, inflammations,
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, stroke, immune deficiencies (e.g. human
 CC immunodeficiency virus (HIV), severe combined immunodeficiency or
 CC infections), autoimmune disorders (e.g. rheumatoid arthritis, Guillain-
 CC Barre syndrome or graft-versus-host disease), cancers (e.g. thyroid
 CC cancer, lung cancers, small cell carcinoma, Kaposi's sarcoma, brain
 CC tumours, prostate cancer, ovarian cancer or leukaemias), or inflammatory
 CC disorders (e.g. inflammatory bowel disease or Crohn's disease). The
 CC polynucleotides and proteins are useful for screening peptides or small
 CC molecule inhibitors or agonists that are useful for treating these
 CC diseases. The polypeptide is also useful as molecular markers, or as a
 CC food supplement. The present sequence is a cytokine or cell
 CC proliferation/differentiation-related protein of the invention
 XX
 SQ Sequence 142 AA;

Query Match 15.8%; Score 163.5; DB 6; Length 142;
 Best Local Similarity 26.1%; Pred. No. 2.1e-08;
 Matches 40; Conservative 25; Mismatches 67; Indels 21; Gaps 5;
 QY 38 LVMVALGLTLVILMSLLLYQRTLCGSGKGFMCSCRCFNLWMRNGSHCYFYSMEKRDWN 97
 DB 3 VLLAVSGVIVVLASR-----AGAR-----CQCPGPGWVLSSEHCYFYSAAQAW 48
 QY 98 SSLKFCADKSGHLLTFPDNQGNVLFQFYVGDYFVIGL-RDIDGWRWEDGPALSIL-- 154
 DB 49 ASQAFCSAYHATLPLLSHTQ--DFLGRYPVSRHSWVGAWRPGQWHWIDEAPLPQLLPE 106
 QY 155 --SNSVQKCGTIHRCGHHASCEVALQWICEK 185
 DB 107 DGEDNLDINCALBEGTLVAANCSTPRPFWCAK 139

RESULT 14

AAM80302

ID AAM80302 standard; protein; 160 AA.

XX AAM80302;

XX

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:44:06 ; Search time 39.5 Seconds
(without alignments)
1492.972 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSTLELPAAAPRVQD.....GLHASCEVALQWICEKVLIP 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 724942

Minimum DB seq length: 0
Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	1036	100.0	188	9	US-09-811-367B-5	Sequence 5, Appli
2	838	80.9	188	9	US-09-811-367B-3	Sequence 3, Appli
3	170	16.4	165	10	US-09-759-130B-98	Sequence 98, Appli
4	170	16.4	165	16	US-10-741-790-98	Sequence 98, Appli
5	167.5	16.2	161	10	US-09-766-511B-55	Sequence 55, Appli
6	164.5	15.9	182	9	US-09-764-870-310	Sequence 310, Appl
7	164.5	15.9	182	14	US-10-125-540-310	Sequence 310, Appl
8	163	15.7	145	10	US-09-759-130B-108	Sequence 108, Appl
9	163	15.7	145	16	US-10-741-790-108	Sequence 108, Appl
10	161	15.5	181	13	US-10-114-893-22	Sequence 22, Appli
11	160	15.4	162	14	US-10-270-470-2	Sequence 2, Appli
12	159.5	15.4	188	10	US-09-759-130B-83	Sequence 83, Appli
13	159.5	15.4	188	16	US-10-741-790-83	Sequence 83, Appli
14	155	15.0	132	15	US-10-335-009-4	Sequence 4, Appli
15	155	15.0	179	10	US-09-919-039-130	Sequence 130, Appl

16	155	15.0	179	15	US-10-335-009-10	Sequence 10, Appl
17	154	14.9	138	10	US-09-759-130B-100	Sequence 100, App
18	154	14.9	138	16	US-10-741-790-100	Sequence 100, App
19	154	14.9	162	10	US-09-759-130B-85	Sequence 85, Appl
20	154	14.9	162	16	US-10-741-790-85	Sequence 85, Appl
21	153.5	14.8	140	9	US-09-764-870-340	Sequence 340, App
22	153.5	14.8	140	9	US-09-764-870-486	Sequence 486, App
23	153.5	14.8	140	14	US-10-125-540-340	Sequence 340, App
24	153.5	14.8	140	14	US-10-125-540-486	Sequence 486, App
25	153.5	14.8	149	10	US-09-284-320-11	Sequence 11, Appl
26	153.5	14.8	149	13	US-10-114-893-32	Sequence 32, Appli
27	153.5	14.8	149	14	US-10-088-859-2	Sequence 2, Appli
28	153.5	14.8	149	14	US-10-179-528-1	Sequence 1, Appli
29	153	14.8	133	12	US-10-239-656-3	Sequence 3, Appli
30	153	14.8	143	12	US-10-239-656-2	Sequence 2, Appli
31	153	14.8	162	12	US-10-239-656-90	Sequence 90, Appli
32	153	14.8	187	10	US-09-759-130B-86	Sequence 86, Appl
33	153	14.8	187	16	US-10-741-790-86	Sequence 86, Appl
34	153	14.8	187	16	US-10-775-640-12	Sequence 12, Appl
35	147.5	14.2	94	9	US-09-764-870-466	Sequence 466, App
36	147.5	14.2	94	14	US-10-125-540-466	Sequence 466, App
37	146.5	14.1	149	9	US-09-944-807-6	Sequence 6, Appli
38	146	14.1	146	12	US-10-296-115-1275	Sequence 1275, Ap
39	145	14.0	117	10	US-09-759-130B-110	Sequence 110, App
40	145	14.0	117	16	US-10-741-790-110	Sequence 110, App
41	144.5	13.9	119	9	US-09-764-870-302	Sequence 302, App
42	144.5	13.9	119	14	US-10-125-540-302	Sequence 302, App
43	144	13.9	137	14	US-10-106-698-5855	Sequence 5855, Ap
44	142	13.7	124	12	US-09-964-956-67	Sequence 67, Appl
45	142	13.7	124	12	US-10-072-012-836	Sequence 836, App

ALIGNMENTS

RESULT 1

US-09-811-367B-5
; Sequence 5, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; PRIOR FILING DATE: 2002-03-12
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-811-367B-5

Query Match	100.0%;	Score 1036;	DB 9;	Length 188;
Best Local Similarity	100.0%;	Pred. No. 2.7e-99;		
Matches 188;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MADNSIYSTLELPAAAPRVQDSSRWKAVLHPCVSYLVNVALGLLTIVILMSLLIYQRTL	60	
Db	1	MADNSIYSTLELPAAAPRVQDSSRWKAVLHPCVSYLVNVALGLLTIVILMSLLIYQRTL	60	
Qy	61	CCSGKGFMCQSCRPNLWNRNGSHCVYFSEMEKDNWSSLKFCADKSHLLTFFPDNGOVN	120	
Db	61	CCSGKGFMCQSCRPNLWNRNGSHCVYFSEMEKDNWSSLKFCADKSHLLTFFPDNGOVN	120	
Qy	121	LFQEVGDEFWIGLRIDIGRWEDGFPALSLISLSNSVQKGTIHRCGLHASCEVALQ	180	
Db	121	LFQEVGDEFWIGLRIDIGRWEDGFPALSLISLSNSVQKGTIHRCGLHASCEVALQ	180	


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Matches 45; Conservative 25; Mismatches 56; Indels 32; Gaps 6;
Qy 40 MVALGLTIVL-----MSL-LYQRTLCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKR 94
   : ||: |: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 5 MIISGLIVVVLKVGMTFLLY-----FCPKDWBFYQARCFELSTSES 47
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 95 DWNSSLKFCADKSGHLLTFDPNQGNLFQEVVGDEDFYWGIGL---RDIDGWRWEDGPPALS 151
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 48 SWNESRDFCKGKSTLAIVNTPDKLFQDITDAEKYFGLIYHREKRWKRWNNVSFNG 107
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 152 SILNSVSVQKQTHRQGL-----HASSCEVALQWICEK 185
   : : : : : : : : : : : : : : : : : : : : : :
Db 108 NVTNQNFNCATI---GLAKTFDAASCDISYRICEK 142
   : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-10-114-893-22
; Sequence 22, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 22
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-22

Query Match 15.5%; Score 161; DB 13; Length 181;
Best Local Similarity 26.2%; Pred. No. 1.8e-08;
Matches 42; Conservative 27; Mismatches 67; Indels 24; Gaps 6;
Qy 37 YLVNVALGLTIVLMSLL--LYQRTLCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKR 94
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 30 FLIM-----FLTIIYCGMVAALSAIRANCHQBPSPVCLQAA--CPESWIGFQRKCFYSDDTK 84
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 95 DWNSSLKFCADKSGHLLTFDPNQGNLFQEVVGDEDFYWGIGL---RWEDG----- 146
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 85 NWTSSQRFCSQDADLAQVESQFELNLLRYKGFSDHWIGLSRQGGQPKWINGTETWTRQ 144
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 147 -PALSLSILNSVSVQKQTHRQGLHASSCEVALQWICEK 185
   : : : : : : : : : : : : : : : : : : : : : :
Db 145 FPILAG-----ECAYLNKDGASSARHYTERKWCISK 176
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RESULT 11
US-10-270-470-2
; Sequence 2, Application US/10270470
; Publication No. US20030162955A1
; GENERAL INFORMATION:
; APPLICANT: Chalus, Lionel
; APPLICANT: Quan, Ahn B.
; APPLICANT: Bates, Elizabeth Ester Mary
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Saeland, Sem
```

```
; APPLICANT: Lebecque, Serge J.E.
; APPLICANT: Phillips, Joseph H.
; TITLE OF INVENTION: ISOLATED MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
; FILE REFERENCE: DX0802QK
; CURRENT APPLICATION NUMBER: US/10/270,470
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: US 09/270,368
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: US 60/078,334
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-270-470-2

Query Match 15.4%; Score 160; DB 14; Length 162;
Best Local Similarity 34.0%; Pred. No. 2e-08;
Matches 34; Conservative 15; Mismatches 47; Indels 4; Gaps 2;
Qy 50 LMSLLYQRTLCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKRDWNSSLKFCADKSGH 109
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 54 LSELHSYHSSLTCTFSGTKVPAMGCPASWKSFGSSCYFISSEKVKWSKSEQNCVEMGAH 113
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 110 LITFPDQGNLFQEVVGEDF-YWIGLRDIDG---WRWED 145
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 114 LVVFTEAEQNFIQQQLNESFYFLGLSLDPQGNNNWQWID 153
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 12
US-09-759-130B-83
; Sequence 83, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Sharp, John D.
; APPLICANT: Barnes, Thomas S.
; APPLICANT: Kirst, Susan J.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Myers, Paul S.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USRS.
; FILE REFERENCE: MP100-5350MIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
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; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-83

Query Match 15.4%; Score 159.5; DB 10; Length 188;
Best Local Similarity 25.5%; Pred. No. 2.6e-08;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;
QY 40 MVALGLLTIVL-----MSLLL-----YQRTLCGGS-----KGEMCS 70
Db 5 MIISGLIVVLKVVGMTLFLFYPOIFNKNSNDGFTTTSYGYVSQIFGSSSPNGFIT 64
QY 71 QC--SRCNLMWRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVNLFQYVGE 128
Db 65 RSYGTVCPKDMFEFYQARCFLLSTSESSWNESRDFCKGKGSTLAIVNTPKLFQDITDA 124
QY 129 DFYWTGL--RDIDGRWEDGPAISLSILSNVSVKCGTIHRCGL-----HASSCEVALQW 181
Db 125 EKIFYGLIYHREKRWNNINNVFNQNTNQNFCATI---GLTKTFDAASCDISYRR 181
QY 182 ICEK 185
Db 182 ICEK 185

RESULT 13

US-10-741-790-83
; Sequence 83, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/10/741,790
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19

; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-790-83

Query Match 15.4%; Score 159.5; DB 16; Length 188;
Best Local Similarity 25.5%; Pred. No. 2.6e-08;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;
QY 40 MVALGLLTIVL-----MSLLL-----YQRTLCGGS-----KGEMCS 70
Db 5 MIISGLIVVLKVVGMTLFLFYPOIFNKNSNDGFTTTSYGYVSQIFGSSSPNGFIT 64
QY 71 QC--SRCNLMWRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVNLFQYVGE 128
Db 65 RSYGTVCPKDMFEFYQARCFLLSTSESSWNESRDFCKGKGSTLAIVNTPKLFQDITDA 124
QY 129 DFYWTGL--RDIDGRWEDGPAISLSILSNVSVKCGTIHRCGL-----HASSCEVALQW 181
Db 125 EKIFYGLIYHREKRWNNINNVFNQNTNQNFCATI---GLTKTFDAASCDISYRR 181
QY 182 ICEK 185
Db 182 ICEK 185

RESULT 14

US-10-335-009-4
; Sequence 4, Application US/10335009
; Publication No. US20040001804A1
; GENERAL INFORMATION:
; APPLICANT: Porunelloor, Mathew A.
; APPLICANT: Boles, Kent S.
; TITLE OF INVENTION: ILT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE: 11707.02/469687-7
; CURRENT APPLICATION NUMBER: US/10/335,009
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-009-4

Query Match 15.0%; Score 155; DB 15; Length 132;
Best Local Similarity 27.1%; Pred. No. 5.1e-08;
Matches 36; Conservative 20; Mismatches 59; Indels 18; Gaps 4;
QY 62 CGSKGFMCSCQSRCPNLMWRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVN 121
Db 4 CHQEPSVCLQAA--CPESWIGFQRCFYFSDTKWTSORFCDSDQADLAQVESFOELNF 62
QY 122 FQYVGBDFYWIGLRIDIG--WRWEDG-----PALSLSILSNVSVKCGTIHRCGLHA 172
Db 63 LLRYKGPSDHWIGLSREQGGPWKINGTWRQFPILGAG-----GCAYLNDKGASS 114
QY 173 SSCEVALQWICEK 185
Db 115 ARHYTGKRWICSK 127

RESULT 15

US-09-919-039-130
; Sequence 130, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.

; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 130
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CD1
US-09-919-039-130

Query Match 15.0%; Score 155; DB 10; Length 179;
Best Local Similarity 27.0%; Pred. No. 7.3e-08;
Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;

Qy	24	WK-VKAVLHRCVSYLVNVALGLITVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLMW	80
Db	9	WRLISGTLGIICLS--LMATLGIILKNSFTKLSIEPAFTGPNIELQKDSDCSCQEKW	66
Qy	81	RNGSHCYFFSMEKEDWNSLKFCDKGSLLLTTPDNOGVNLFQYVGEDFYWGL---RD	137
Db	67	GYRCNCYFISSEQKTWNEHRHLCASQKSLQLQNTDELDFMSS--SQQFYWGLSYSEE	124
Qy	138	IDGWRWEDGPALSLILNSV---VQKCGTHRCG-LHASSCEVALOWICEKVL	187
Db	125	HTAWLWENGSAISQYLPSPFTFTKNCIAYNPNGNALDESCEDKNRYICKQQL	178

Search completed: August 10, 2004, 16:53:37
Job time : 39.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:40:40 ; Search time 14.5 Seconds
(without alignments)
669.357 Million cell updates/sec

Title: US-09-811-367B-5

Perfect score: 1036

Sequence: 1 MADNSYSLLELPAAARVQD.....GLHSSCEVALQWICEKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 303002

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1036	100.0	188	3	US-08-722-126A-5
2	1036	100.0	188	5	PCT-US95-04258-5
3	651	62.8	114	3	US-08-722-126A-6
4	651	62.8	114	5	PCT-US95-04258-6
5	273	26.4	76	4	US-09-531-056A-23
6	166.5	16.1	115	3	US-08-722-126A-8
7	166.5	16.1	115	5	PCT-US95-04258-8
8	158.5	15.3	167	3	US-08-772-440-21
9	155	15.0	179	1	US-08-690-095-9
10	155	15.0	179	2	US-08-650-578-2
11	155	15.0	179	2	US-08-688-342-3
12	155	15.0	179	2	US-09-113-788-3
13	155	15.0	179	3	US-09-113-789-9
14	153	14.8	122	3	US-08-722-126A-9
15	153	14.8	122	5	PCT-US95-04258-9
16	153	14.8	126	3	US-08-772-440-10
17	153	14.8	134	3	US-08-543-246B-20
18	153	14.8	176	3	US-08-772-440-8
19	153	14.8	180	3	US-08-772-440-31
20	153	14.8	187	4	US-09-127-946-12
21	149.5	14.4	168	3	US-08-772-440-17
22	148	14.3	173	4	US-09-531-056A-4
23	147.5	14.2	79	4	US-09-531-056A-19
24	145.5	14.0	129	3	US-08-722-126A-10
25	145.5	14.0	129	5	PCT-US95-04258-10
26	142	13.7	175	3	US-08-772-440-15
27	140	13.5	78	4	US-09-531-056A-18

Sequence 16, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 23, Appl
Sequence 27, Appl
Sequence 14, Appl
Sequence 22, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 21, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-08-722-126A-5

; Sequence 5, Application US/08722126A

; Patent No. 6034227

; GENERAL INFORMATION:

; APPLICANT: PECHT, Israel

; APPLICANT: GUTHMANN, Marcelo D.

; APPLICANT: TAL, Michael

; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL

; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

; STREET: 419 Seventh Street N.W., Ste. 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/722,126A

; FILING DATE: 08-OCT-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04258

; FILING DATE: 06-APR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 109257

; FILING DATE: 08-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: PECHT=1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 628-5197

; TELEFAX: (202) 737-3528

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 188 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-722-126A-5

Query Match 100.0%; Score 1036; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.3e-105;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLEPAAPRVQDDSRWKVAVLHRRPCVSYLWVALGLLTVILMSLLYQRTL 60
DB 1 MADNSIYSTLEPAAPRVQDDSRWKVAVLHRRPCVSYLWVALGLLTVILMSLLYQRTL 60
QY 61 CCGSGKGFMCSCQRCFNLWNRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVN 120
DB 61 CCGSGKGFMCSCQRCFNLWNRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVN 120
QY 121 LFOEYVGDFFYIGLRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGDFFYIGLRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVL 188
DB 181 WICEKVL 188

RESULT 2

PCT-US95-04258-5

; Sequence 5, Application PC/TU9504258

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL

; FUNCTION-ASSOCIATED ANTIGEN (MAFA)

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04258

; FILING DATE: 06-APR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 109257

; FILING DATE: 08-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: PECHT-1 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 188 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US95-04258-5

Query Match

Best Local Similarity 100.0%; Score 1036; DB 5; Length 188;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLEPAAPRVQDDSRWKVAVLHRRPCVSYLWVALGLLTVILMSLLYQRTL 60
DB 1 MADNSIYSTLEPAAPRVQDDSRWKVAVLHRRPCVSYLWVALGLLTVILMSLLYQRTL 60
QY 61 CCGSGKGFMCSCQRCFNLWNRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVN 120
DB 61 CCGSGKGFMCSCQRCFNLWNRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVN 120

QY 121 LFOEYVGDFFYIGLRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGDFFYIGLRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVL 188
DB 181 WICEKVL 188

RESULT 3

US-08-722-126A-6

; Sequence 6, Application US/08722126A

; Patent No. 6034227

; GENERAL INFORMATION:

; APPLICANT: PECHT, Israel

; APPLICANT: GUTHMANN, Marcelo D.

; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL

; FUNCTION-ASSOCIATED ANTIGEN (MAFA)

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

; STREET: 419 Seventh Street N.W., Ste. 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/722,126A

; FILING DATE: 08-OCT-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04258

; FILING DATE: 06-APR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 109257

; FILING DATE: 08-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: PECHT-1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 628-5197

; TELEFAX: (202) 737-3528

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 114 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-722-126A-6

Query Match

Best Local Similarity 100.0%; Score 651; DB 3; Length 114;

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 CPNLWMRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVNLFQEVYVGDFFYWG 134
DB 1 CPNLWMRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVNLFQEVYVGDFFYWG 60
QY 135 LRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQWICEKVL 188
DB 61 LRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQWICEKVL 114

RESULT 4

PCT-US95-04258-6

Sequence 6, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECTH=1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04258-6

Query Match 62.8%; Score 651; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.7e-64;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 CPNLMWRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTFFPDNGVNLFOEYVGEDFYWIG 134
Db 1 CPNLMWRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTFFPDNGVNLFOEYVGEDFYWIG 60

Qy 135 LRIDGWRWEDGPALSLILSNVQKGTTHRCGLHASCEVALQWICEKVP 188
Db 61 LRIDGWRWEDGPALSLILSNVQKGTTHRCGLHASCEVALQWICEKVP 114

RESULT 5
US-09-531-056A-23
Sequence 23, Application US/09531056A
Patent No. 6455683
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
FILE REFERENCE: DB20 NP
CURRENT APPLICATION NUMBER: US/09/531,056A
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 76
TYPE: PRT
ORGANISM: Homo sapiens
US-09-531-056A-23

Query Match 26.4%; Score 273; DB 4; Length 76;
Best Local Similarity 59.7%; Pred. No. 1.4e-22;
Matches 43; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy 75 CPNLMWRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTFFPDNGVNLFOEYVGEDFYWIG 134
Db 3 CPDWMKYGKNCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSLQVFLSEAFQWIG 62

Qy 135 LRIDGWRWEDG 146
Db 63 LRNMSCWRWEDG 74

RESULT 6
US-08-722-126A-8
Sequence 8, Application US/08722126A
Patent No. 6034227
GENERAL INFORMATION:
APPLICANT: PECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: UNITED STATES OF AMERICA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECTH=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-722-126A-8

Query Match 16.1%; Score 166.5; DB 3; Length 115;
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 31; Conservative 22; Mismatches 57; Indels 3; Gaps 2;

Qy 75 CPNLMWRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTFFPDNGVNLFOEYVGEDFYWIG 134
Db 1 CSEDWVGQKCYFISTVKRSWTSQAACSEHGATLAVIDSEKDMNFKRYAGEEHWVG 60

Qy 135 LRIDG--WRWEDGPALSLILSNVQKGTTHRCGLHASCEVALQWICEK 185
Db 61 LKKEPGHPKWSNGKEFN-NWENVTGSDKCVFLKNTVSSMECEKNLYWICKN 112

RESULT 7

PCT-US95-04258-8
; Sequence 8, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECTH=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04258-8

Query Match 16.1%; Score 166.5; DB 5; Length 115;
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 31; Conservative 22; Mismatches 57; Indels 3; Gaps 2;
QY 75 CPNLMWRNGSHCYFFSMKRDWNSLKFCAKDGSHLLTFPDNQGVNLFQEVYGFYWG 134
Db 1 CSEDWVGQKCYFISTVKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREEHWVG 60
QY 135 LRDIDG--WRWEDGPALSLSILNSVVOVKGTIHRGCLHASCEVALQWICEK 185
Db 61 LKXEPGHPKWSNGKEFN-NWFNVGTGDKCVFLKXNTEVSSMECEKNLYWICNK 112

RESULT 8

US-08-772-440-21
; Sequence 21, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston

STATE: Texas
COUNTRY: USA
ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-21

Query Match 15.3%; Score 158.5; DB 3; Length 167;
Best Local Similarity 28.6%; Pred. No. 1.3e-09;
Matches 44; Conservative 23; Mismatches 66; Indels 21; Gaps 6;
QY 50 LMSLLYQRTLCGSKGFMCSQ-----CSRCPNLMWRNGSHCYFFSMKRDWNSLKFCAK 105
Db 10 LYELHTYHSSLTCTFSEGTWSEKMWGC--CPNHWKSGSCYLSTKFNFWSTSEQNCVQ 67
QY 106 KGSHLLTFPDNQGVNLFQEVYGFDF-YWIGLRDIDG---WRWEDGPALSLSIL-----S 155
Db 68 MGAHLVINTREAEQNFITQQLNESLSYFLGSLSDPGNGKQWQIDDTFSPQVRFWHPHEP 127
QY 156 NSVVOVKGTI-----HRCGLHASCEVALQWICE 184
Db 128 NLPEERCVSIVYWNPSKMGWMDVFCDSKHNSICE 161

RESULT 9

US-08-690-095-9
; Sequence 9, Application US/08690095
; Patent No. 5792648
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,095
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US

Db 9 WRLISGTLGIICLS--LMATLIGILLKNSFTKLSIEPAFTPGPNIELQKSDCCSCQEKW 66
QY 81 RNSHCYFYSMEKRDWNSLKECADKSGSHLLTFPDNQGNLFQEVYGEDFYWIGL---RD 137
Db 67 GYRCNCYFISSEQKWTNESHLCASQKSSLLQNTDELDFMSS--SQQFYWIGLSYSEE 124
QY 138 IDGWRWDGPALSLSLNSV---VQKGTTHRCG-LHASSCEVALQWICEKVL 187
Db 125 HTAWLWENGSAISOYLFPFSEFTNTKNCIAYPNPNGNALDESDCKNRYICKQOL 178
RESULT 12
US-09-113-788-3
; Sequence 3, Application US/09113788
; Patent No. 5969104
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/688,342
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
US-09-113-788-3
Query Match 15.0%; Score 155; DB 2; Length 179;
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;
QY 24 WK-VKAVLHRCVSVLYVMVAGLLTVILMSLLQRTLCCSGKGM--CSQSCRCPNLWM 80
Db 9 WRLISGTLGIICLS--LMATLIGILLKNSFTKLSIEPAFTPGPNIELQKSDCCSCQEKW 66
QY 81 RNSHCYFYSMEKRDWNSLKECADKSGSHLLTFPDNQGNLFQEVYGEDFYWIGL---RD 137
Db 67 GYRCNCYFISSEQKWTNESHLCASQKSSLLQNTDELDFMSS--SQQFYWIGLSYSEE 124
QY 138 IDGWRWDGPALSLSLNSV---VQKGTTHRCG-LHASSCEVALQWICEKVL 187

Db 125 HTAWLWENGSAISOYLFPFSEFTNTKNCIAYPNPNGNALDESDCKNRYICKQOL 178
RESULT 13
US-09-113-789-9
; Sequence 9, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
US-09-113-789-9
Query Match 15.0%; Score 155; DB 3; Length 179;
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;
QY 24 WK-VKAVLHRCVSVLYVMVAGLLTVILMSLLQRTLCCSGKGM--CSQSCRCPNLWM 80
Db 9 WRLISGTLGIICLS--LMATLIGILLKNSFTKLSIEPAFTPGPNIELQKSDCCSCQEKW 66
QY 81 RNSHCYFYSMEKRDWNSLKECADKSGSHLLTFPDNQGNLFQEVYGEDFYWIGL---RD 137
Db 67 GYRCNCYFISSEQKWTNESHLCASQKSSLLQNTDELDFMSS--SQQFYWIGLSYSEE 124
QY 138 IDGWRWDGPALSLSLNSV---VQKGTTHRCG-LHASSCEVALQWICEKVL 187
Db 125 HTAWLWENGSAISOYLFPFSEFTNTKNCIAYPNPNGNALDESDCKNRYICKQOL 178
RESULT 14
US-08-722-126A-9
; Sequence 9, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:

APPLICANT: PECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: UNITED STATES OF AMERICA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/722,126A
APPLICATION NUMBER: US/08-722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1A
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-722-126A-9

Query Match 14.8%; Score 153; DB 3; Length 122;
Best Local Similarity 27.9%; Pred. No. 3.5e-09;
Matches 34; Conservative 22; Mismatches 56; Indels 10; Gaps 4;
Qy 75 CPNLWMRNGSHCYFYSMEKRDWNSLKFCDKAGSHLLTFPDNQGVLNLFQEVVGEDF--YW 132
Db 1 CPQDWLSHRDKCFHVSQVSNWEEGLVDCDGKATMLIQDEELRFLDLSIKEKNSFW 60
Qy 133 IGLR---DIDGWRWEDGPALS---LSILSNVVKCGTTHRCGLHASSCEVALQWICEK 185
Db 61 IGLRYTLPDNM-WKWINGSTLNSDLKITGTENDSCAAISGDKVTFESCNSDNRWICQK 119
Qy 186 VL 187
Db 120 EL 121

RESULT 15
PCT-US95-04258-9
Sequence 9, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1 PCT
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04258-9
Query Match 14.8%; Score 153; DB 5; Length 122;
Best Local Similarity 27.9%; Pred. No. 3.5e-09;
Matches 34; Conservative 22; Mismatches 56; Indels 10; Gaps 4;
Qy 75 CPNLWMRNGSHCYFYSMEKRDWNSLKFCDKAGSHLLTFPDNQGVLNLFQEVVGEDF--YW 132
Db 1 CPQDWLSHRDKCFHVSQVSNWEEGLVDCDGKATMLIQDEELRFLDLSIKEKNSFW 60
Qy 133 IGLR---DIDGWRWEDGPALS---LSILSNVVKCGTTHRCGLHASSCEVALQWICEK 185
Db 61 IGLRYTLPDNM-WKWINGSTLNSDLKITGTENDSCAAISGDKVTFESCNSDNRWICQK 119
Qy 186 VL 187
Db 120 EL 121
Search completed: August 10, 2004, 16:45:20
Job time : 14.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:11:32 ; Search time 32.7823 Seconds
(without alignments)
1819.059 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MTDSVIYSMLPPTAQON.....GLQASSCEVPLHGVCVKVRL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1023	100.0	189	4	O43198
2	1007	98.4	189	4	O75613
3	994	97.2	195	4	Q96E93
4	548.5	53.6	188	11	O88713
5	525.5	51.4	188	11	O64335
6	226	22.1	231	4	Q9NZS2
7	225	22.0	181	4	Q9NZS1
8	222	21.7	200	13	Q802S8
9	219.5	21.5	275	11	Q9D403
10	219	21.4	231	6	Q8MT05
11	210	20.5	227	11	O9WU32
12	210	20.5	231	11	O54872
13	205	20.0	200	6	Q8SPX1
14	201.5	19.7	231	6	Q9MZK3
15	201	19.6	225	4	Q12918
16	201	19.6	233	6	Q8MJH7

17	200	19.6	233	6	Q8MJH6	Q8mjh6 pongo pygma
18	199.5	19.5	207	11	Q8BHH6	Q8bhh6 mus musculus
19	199.5	19.5	231	6	Q9GK88	Q9gk88 macaca mula
20	199.5	19.5	269	11	Q9D676	Q9d676 mus musculus
21	199	19.5	196	11	Q8VI21	Q8vi21 mus musculus
22	199	19.5	233	6	Q8MJT0	Q8mjt0 pongo pygma
23	199	19.5	233	6	Q9MYM6	Q9nym6 pan troglod
24	197	19.3	232	11	O54709	O54709 mus musculus
25	196.5	19.2	246	6	Q9MZK2	Q9mzk2 macaca mula
26	196	19.2	211	11	Q91ZW5	Q91zw5 mus musculus
27	196	19.2	246	6	Q9MZK1	Q9mzk1 macaca mula
28	195.5	19.1	244	11	Q9Z202	Q9z202 mus musculus
29	195.5	19.1	278	6	Q9XTA8	Q9xta8 oryctolagus
30	194.5	19.0	178	11	Q91ZW9	Q91zw9 mus musculus
31	194	19.0	233	6	Q8MJH5	Q8mjh5 pongo pygma
32	193	18.9	233	6	Q8MJH8	Q8mjh8 pongo pygma
33	193	18.9	233	6	Q8MJH9	Q8mjh9 pongo pygma
34	193	18.9	257	13	Q90636	Q90636 gallus gall
35	193	18.9	270	6	P79391	P79391 bos taurus
36	192.5	18.8	208	11	Q91ZW7	Q91zw7 mus musculus
37	192.5	18.8	244	11	Q9WU31	Q9wu31 mus musculus
38	192	18.8	236	6	Q95L94	Q95l94 macaca mula
39	191.5	18.7	230	11	O54871	O54871 rattus norv
40	190	18.6	199	6	Q95MQ1	Q95mq1 bos taurus
41	190	18.6	227	11	Q61973	Q61973 mus musculus
42	190	18.6	233	6	Q8MJ11	Q8mj11 pongo pygma
43	189.5	18.5	179	6	Q8MJ13	Q8mj13 pongo pygma
44	189.5	18.5	179	6	Q8MHY8	Q8mhy8 pongo pygma
45	189	18.5	216	6	Q8MJH0	Q8mjh0 pongo pygma

ALIGNMENTS

RESULT 1

O43198 ID O43198 PRELIMINARY; PRT; 189 AA.
AC O43198
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Mast cell function-associated antigen.
GN MAF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98438735; PubMed=9765598;
RA Lamers M.B., Lamont A.G., Williams D.H.;
RT "Human MAF has alternatively spliced variants.";
RL Biochim. Biophys. Acta 1399:209-212(1998).
DR ENBL, AF034952; AAC34731.1; -
DR GO; GO:006021; C-integrin to membrane; TAS.
DR GO; GO:0003793; F:defense/immunity protein activity; TAS.
DR GO; GO:0005530; F:lectin; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT. 1.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 189 AA; 21079 MW; 15E042AD40B2B4F6 CRC64;

Query Match 100.0%; Score 1023; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 7.4e-105;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDSVIYSMLPPTAQONDYGPQKSSSSKSPSCSLVAITGLLTAVLLSVLLYQWIL 60

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Db 1 MTDSVIYSMLPLPTATQNDYGPQKSSSKPSCSLVAITGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
QY 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
Db 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
QY 181 HGVCKKVRLL 189
Db 181 HGVCKKVRLL 189

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RESULT 2

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O75613 PRELIMINARY; PRT; 189 AA.
AC O75613;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ITIM-containing receptor MAFA-L.
GN MAFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Butcher S., Arney K.L., Cook G.P.;
RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene
RT complex and expressed by basophils and NK cells.";
RL Eur. J. Immunol. 28:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
DR EMBL; AF081675; AAC32200.1; -
DR EMBL; AF097358; RAD03719.1; -
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

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Query Match 98.4%; Score 1007; DB 4; Length 189;
Best Local Similarity 98.4%; Pred. No. 4.3e-103;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDSVIYSMLPLPTATQNDYGPQKSSSKPSCSLVAITGLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYSMLPLPTATQNDYGPQKSSSKPSCSLVAITGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
QY 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
Db 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
QY 181 HGVCKKVRLL 189
Db 181 HGVCKKVRLL 189

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RESULT 3

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Q96E93 PRELIMINARY; PRT; 195 AA.
AC Q96E93;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Similar to killer cell lectin-like receptor subfamily G, member 1.
DE 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Strausberg R.;
RL EMBL; BC012621; AAHL2621.1; -
DR GenBank; HGNC:6380; KLRG1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 195 AA; 21831 MW; 178EE98E08EBC473 CRC64;

Query Match 97.2%; Score 994; DB 4; Length 195;
Best Local Similarity 98.4%; Pred. No. 1.2e-101;
Matches 183; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDSVIYSMLPLPTATQNDYGPQKSSSKPSCSLVAITGLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYSMLPLPTATQNDYGPQKSSSKPSCSLVAITGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
QY 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
Db 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
QY 181 HGVCKK 186
Db 181 HGVCKK 186

RESULT 4
O88713 PRELIMINARY; PRT; 188 AA.
AC O88713;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-AUG-1999 (TREMELrel. 11, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).
DE 1.
GN KLRG1 OR MAFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17 SCID;
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
RN [2]

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RP SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN=129/SvevTACFB; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=11220622;
RA Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor G1 gene (KLRF1), the mouse homologue
RT of MAFA.";
RL Immunogenetics 52:206-211(2001).
RL EMBL; AF097357; AAD03718.1; -.
DR EMBL; AJ010751; CAA09342.1; -.
DR EMBL; AF317727; AA40082.1; -.
DR MGD; MGI:1355294; Klrg1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match 53.6%; Score 548.5; DB 11; Length 188;
Best Local Similarity 55.6%; Pred. No. 2.1e-52;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDVSYMLELPTATQAQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MADSSYSTLELPEAPQVQDSRWKLVKAVLRHLSFAMVALLGLTVILMSILMYQRII 60

QY 61 CQGSNTSTCASCPSPDRMKYGNHCYFVSVEKDNSSLEFCIARDSHLLVITDQEMS 120
Db 61 CCGSKDSTCHSCPILTRNGSHCYFYSMEKRDWNSLKFCADKSHLLTFPDNQGVK 120

QY 121 LLQVFLSEAFCWIGLRNNGWRWEDGSPINFSISSNFVOTCGAINKNGLOASSCEVPL 180
Db 121 LFGEYLGDDFYWIGLRNIDGWRWEGGPAISL-RILTNSLQRCGAIRNGLOASSCEVAL 179

QY 181 HGVCCKV 187
Db 180 QWICKV 186

RESULT 5
Q64335 PRELIMINARY; PRT; 188 AA.
AC Q64335;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MAFA protein.
GN MAFA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=Testis;
RA Bocke Jr P., Guthmann M.D., Pecht I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=96016176; PubMed=7568140;
RA Guthmann M.D., Tal M., Pecht I.;
RT "A secretion inhibitory signal transduction molecule on mast cells is
RT another C-type lectin.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL; X97191; CAA65829.1; -.

SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN=129/SvevTACFB; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=11220622;
RA Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor G1 gene (KLRF1), the mouse homologue
RT of MAFA.";
RL Immunogenetics 52:206-211(2001).
RL EMBL; AF097357; AAD03718.1; -.
DR EMBL; AJ010751; CAA09342.1; -.
DR EMBL; AF317727; AA40082.1; -.
DR MGD; MGI:1355294; Klrg1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match 51.4%; Score 525.5; DB 11; Length 188;
Best Local Similarity 53.5%; Pred. No. 7.2e-50;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDVSYMLELPTATQAQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MADNSYSTLELPAAPRVQDDSRWKVAVLRHFCVSLVWVALLGLTVILMSULLYQRTL 60

QY 61 CQGSNTSTCASCPSPDRMKYGNHCYFVSVEEKNSSLEFCIARDSHLLVITDQEMS 120
Db 61 CCGSKGFMCSQCSCPCENLWENGSHCYFYSMEKRDWNSLKFCADKSHLLTFPDNQGVN 120

QY 121 LLQVFLSEAFCWIGLRNNGWRWEDGSPINFSISSNFVOTCGAINKNGLOASSCEVPL 180
Db 121 LFGEYVGDDFYWIGLRIDGWRWEDGPAISLS-ILNSVYVQKGTTHRCGLHASSCEVAL 179

QY 181 HGVCCKV 187
Db 180 QWICKV 186

RESULT 6
Q9NZS2 PRELIMINARY; PRT; 231 AA.
AC Q9NZS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lentin-like receptor F1 (Activating coreceptor NKp80).
GN KLRF1 OR ML/KLRF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KLRF1, a novel member of the killer cell lectin-like receptor
RT gene family; molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
RN [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=21150889; PubMed=11265639;
RA Vitale M., Falco M., Castriconi R., Parolini S., Zambello R.,
RA Sennezato G., Biassoni R., Bottino C., Moretta L., Moretta A.;
RT "Identification of NKp80, a novel triggering molecule expressed by
RT human natural killer cells.";
RL Eur. J. Immunol. 31:233-242(2001).
DR EMBL; AF175206; AAF37804.1; -.
DR EMBL; AJ305370; CAC29425.1; -.
DR Genew; HGNC:13342; KLRF1.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; Lectin_C.

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Db 62 KGFPSPPEKLIAGTLGLICFLVLIIVAVVVITTVATPYINVTYLTSSAQPCPCPKEMISYSHN 121
Qy 86 CYFESVERKWNSSLEFCLARDSHLLVITDQMSLLQVFLSEAFWCIG-IRNNSG--WR 142
Db 122 CYFTIGMERKSWNDLSVCSIKNCSLLYIDSEEQDFLQSL--SLISWTGILRKGRGPWV 179
Qy 143 WEDSGPLNFSIRSSNSFVQ-----TCGAINKNGIQAASSCEVPLHGVCCK 185
Db 180 WKEDS-----IFPKIAEILHDECNCAMMSASGLTADNCTYTLHPYLCK 222

RESULT 12
Q54872 PRELIMINARY; PRT; 231 AA.
AC 054872
AC 054872
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Natural killer cell protein group 2-A (Fragment).
GN NKG2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F344;
RX MEDLINE=98180346; PubMed=9521051;
RA Berg S.F., Dissen E., Westgaard I.H., Fossum S.;
RT "Molecular characterization of two genes in the rat homologous to
RT human NKG2."
RL Eur. J. Immunol. 28:444-450(1998).
DR EMBL; AF021350; AAC40050.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF000059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
FT NON TER 1
SQ SEQUENCE 231 AA; 26335 MW; FF2AB6D33EF2CE99 CRC64;

Query Match 20.5%; Score 210; DB 11; Length 231;
Best Local Similarity 29.0%; Pred. No. 6.9e-15;
Matches 54; Conservative 25; Mismatches 81; Indels 26; Gaps 5;

Qy 24 PQKSSSKPKSCSC-----LVAITLGLTAVLLSVLL-----YQWILCOGSNY 66
Db 43 PSQEQTRICRDCCKGKGFPPPEKLIAGTLGLFISFLVIAVVVITTVATPYTETKAQINS 102
Qy 67 ST-----CASCPCDPRWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQMSLL 122
Db 103 MTRTYQARPCTRCPDDWISYSHNCYIISVERKSWNDGLTSCIKNCSLLHDSIEEQAPL 162
Qy 123 QVFLSEAFWCIGLRNNS---GWRWEDGSLNFSRISNSFVTCGAINKNGIQAASSCEVP 179
Db 163 QSF--SLYSWTGFFPKRSQPPVWENGSTFKPKITTEMLHDEYNCIMMSTSGLTAE NCITL 220

Qy 180 LHGVCK 185
Db 221 HPYVCK 226

RESULT 13
Q8SPX1 PRELIMINARY; PRT; 200 AA.
AC Q8SPX1
AC Q8SPX1
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Type II membrane protein CD69.
OS Sus scrofa (Pig).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Yim D., Sotiriadis J., Kim K.-S., Shin S.-C., Jie H.-B.,
RA Rothschild M.F., Kim Y.B.;
RT "Molecular cloning, expression pattern, and chromosomal mapping of pig
RT CD69."
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF484233; AAL91546.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF000059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 200 AA; 22257 MW; C55E8767E163A57C CRC64;

Query Match 20.0%; Score 205; DB 6; Length 200;
Best Local Similarity 29.6%; Pred. No. 2.1e-14;
Matches 56; Conservative 27; Mismatches 84; Indels 22; Gaps 9;

Qy 13 PTAQAQNDYCP-----QKSSSKP-SCSC--LVAITLGLTAVLLSVLLQWILCOGSN 65
Db 16 PNRGQPSNATGPHFATHHEGSLQVPIPCAVVNVVITVLIITLIALTSVGQYN---CPGOY 72
Qy 66 YSTCAS---CPSCDPRWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOE-MSL 121
Db 73 VPSVPSNMHVSSCPDDWIGYQTKYFISKYKNWTLAQSFCKKHGATLALLESKEDMVF 132
Qy 122 LQVFLSEAFWCIGLRNNSG--WRWEDGSLN--FSRISNSFVTCGAINKNGIQAASSCE 177
Db 133 LKHQVGRAEHWIGLKNEDGQTKWKSNGKEFNWPKLTGS----KNCPLNSTEVSMECE 188
Qy 178 VPLHGVCCK 186
Db 189 KNLHWICSK 197

RESULT 14
Q9WZK3 PRELIMINARY; PRT; 231 AA.
AC Q9WZK3
AC Q9WZK3
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NKG2-C.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20322487; PubMed=10866118;
RA LaBonte M.L., Levy D.B., Letvin N.L.;
RT "Characterization of rhesus monkey CD94/NKG2 family members and
RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,
RT and D."
RL Immunogenetics 51:496-499(2000).
DR EMBL; AF190937; AAF74533.1; -.
DR HSP; P22897; LEGS.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 231 AA; 26107 MW; COD307ABE0262DBD CRC64;

Query Match 19.7%; Score 201.5; DB 6; Length 231;
Best Local Similarity 29.8%; Pred. No. 6e-14;
Matches 59; Conservative 30; Mismatches 92; Indels 17; Gaps 7;

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```
QY 2 TDSVIYSMLELPTAQAQNDYGPQ--KSSSSKPSCLVAITLGLTAVLLSVLLYQWI 59
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
34 TEQEIP-QVENLQNPVNHQGDQIYDCQGLLPPPEKLTAEVLGIICIVIMATVLTVV 92
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 LC---QGSNYS-----TCASCPSPDRMKYGNHCYFVSVEEKDWNSSLEFCLARDSHL 110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
93 LIPPEQSSNLSNTRTKVRHCGHCPPEWITYNSCYIIGKXRTWAESLLACTSKNSSL 152
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 LVITDQEMSLLOVFLSEAFWIGL-RNNSGWRWEDGSPINFRISNS--FVQTGCAIN 167
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
153 LSIDNEEMKFLTAILPSS--WIGVERNSHHPWVTINGLTFKHEIKNSDNASHNCAMLH 210
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 168 KNGLOASSCEVPLHGVCCK 185
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
211 ARGKSNQCESTVIYHCK 228
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 15

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Q12918
ID Q12918 PRELIMINARY; PRT; 225 AA.
AC Q12918;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE HNK-R-Pla protein.
GN HNK-R-Pla.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94358407; PubMed=8077657;
RA Lanier L.L., Chang C., Phillips J.H.;
RT "Human NKR-P1A: A disulfide-linked homodimer of the C-type lectin
RT superfamily expressed by a subset of NK and T lymphocytes.";
RL J. Immunol. 153:2417-2428(1994).
DR EMBL; U11276; AAA21605.1; -.
DR PIR; I38700; I38700.
DR HSSP; P05140; ZAFP.
DR Genew; HGNC:6373; KLRB1.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005530; F:lectin; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 225 AA; 25415 MW; 01BFA925445B93B0 CRC64;
```

```
Query Match 19.6%; Score 201; DB 4; Length 225;
Best Local Similarity 26.0%; Pred. No. 6.6e-14;
Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTDSVIYSMLELPTAQAQNDYGPQKSSSKP-----SCSCLVAITLG 44
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MDQQAITYAELNLPT-----DSGPSSSPSLPRDVCQGSFHWQFALKLSCAGIILLVL- 53
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 45 LLTAVLLSVLLYQWILCOGSNYSTCA-----SCPSPDRMKYGNHCYFVS 90
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
54 VTGLSVST-----SLIQKSIKCSVDIQQRNKTTERPELLNCPYWOQLREKCLLFS 109
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 91 VEEKDWNSSLEFCLARDSHLITDQEMSLLOVFLSE--AFCWIGLR--NNSGWRWED 145
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
110 HTVNPWNNSLADCSKESLLLRDKDLHTQNLIRDKAILFWIGLNFSLSEKNWKNIN 169
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 146 GSPINFS--RISNSFVQTGCAINKNGLOASSCEVPLHGVCCK 186
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
170 GSFINGNDLEIRDAKENSICISISQTSVSYGCGSTEIRWICQK 212
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Job time : 33.7823 secs

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